

QY 1138 CAGCTCCTCAGCAGCAGAACCAGCTTCTCTCTGGAGAGGCAGAGCCTGTCCGAAGAGGTG 1197

```
Db      21 GlnLeuLeuSerLySGlnAenGlnLeuLeuGlnLyrGlnSer-CysArgLySArgTr 40
Qy      1198 GACCGGCTGGGAGCCAGTACCAGCATGCCAATCTGATTTGCTGACCTGATGGA 1255
         |||
Db      40 pthrgLyCySGLyProSerLyThrAlaCySHisAsnLeuIleAlaAspLeuSerGly 59

RESULT 2
US-09-914-259-11
; Sequence 11, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Les
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 3878
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-914-259-11

Alignment Scores:
Pred. No.:      1,05e-15      Length:      3878
Score:          264.00      Matches:      121
Percent Similarity: 40.37%      Conservative: 107
Best Local Similarity: 21.33%      Mismatches: 162
Query Match:      9.65%      Indels:      172
DB:              4          Gaps:      22

US-09-502-945-1 (1-1552) x US-09-914-259-11 (1-3878)
Qy      1 CTCTCGATGCATTCGAGAACTGAAACTTACTTATGAGAGAAAGTGTGA--ATTGAG 57
         |||
Db      1822 MetLeuAsnIleSerSerArgLeuGlnAlaAlaValGlnLyrSerLeuGlnAlaIleSer 1841
Qy      58 GAA-----TCCCAATTTGAAGTTTGGAGAAAGAC 87
         |||
Db      1842 GlnThrSerSerGlnLeuGlnHisAlaLysValThrGlnThrGlnLeuMetArgGlnSer 1861
Qy      88 TTAGCTGATATATGACAGAACTTGAGATCTTGAAGCACTAAAGCATTAAGAATTT 147
         |||
Db      1862 PheArgGlnLyrSerGlnLyrAlaThrGlnLyrSerLyrSerGlnGlnLyrLeuArgGlnLyr 1881
Qy      148 CTTCGGCTGCTTAIACCTTGAACCGTGTGTGTCTTTGTTGAATGCTCAGCAT 207
         |||
Db      1882 LeuHisGlnLyrSerArgAlaArgGln-----GlnLeuAlaValGlnLeuSerLysAla 1899
Qy      208 GAAGCTGTCTTCTCCCAACCCATACATATGTCATATGCAAGCAATCGAAGACTGTT 267
         |||
Db      1900 GlnGlyValIleAspGlyTyrAlaAspGlnLyrThrLeu-----PheGlnLyrGlnIle 1917
Qy      268 AAAGAAAGATGATCATTTGATGTCACATA-----GTTCCGTAAG 309
         |||
Db      1918 GlnGlnLyrThrAspIleIleAspArgLeuGlnGlnLyrLeuLeuSerLysAlaSerAsnArg 1937
Qy      310 AGCAGCTGGCAGATACGACCAAGA----- 336
         |||
Db      1938 LeuGlnLyrLeuGlnAlaGlnGlnGlnGlnIleGlnGlnLyrGlnLyrGlnLyrLeuSerArg 1957
Qy      337 -----GAAGCAAGTCTTATGAACAGCGGAACCAAGTTTTCGA 375
         |||
Db      1958 GlnLyrSerGlnLyrMetLysAlaGlnLyrAlaGlnLyrProValGlnGln-----GlnLeuLeuGln 1975
Qy      376 ATATCTGAGAGAGCATTGTTGAATAAACAAGGCTTAACTCAGTGTGACAGTTGAG 435
         |||
Db      1976 GlnThrGlnLyrSerLeuMetLysGlnLyrSerLeuGlnValGlnLyrSerGlnAlaGlnLyrValArg 1995
Qy      436 AAGAGCTGAGAGAGGAGCGGAGAGCACTGAAAAAGAACTTGATCTCAG----- 486
```

```
Db      1996 AspArgLeuGlnLyrSerGlnValLysAlaLeuGlnLyrIleAspValGlnGlnValLysArg 2015
Qy      487 -----CAAGAGAAAAGGCCATTGAGAAAAGACATG----- 516
         |||
Db      2016 PheIleGlnLyrGlnGlnGlnLyrSerThrGlnLyrMetAspLeuLyrGlnGlnGlnGln 2035
Qy      517 -----ATGAAAAGGAAATTAAGAAAGAGGATGATGCGATCAAGATGTTG----- 567
         |||
Db      2036 AlaLeuGlnLyrSerGlnLyrSerMetArgLysPheLeuLyrSerGlnGlnAlaIleAspArg 2055
Qy      568 -----ATCTGTCTCAGAAATATGTCGCCAATGCACTGGAGCCGAGTGAAG 612
         |||
Db      2056 GlnHisGlnLyrAspValPheGlnGlnGlnLyrIleGlnLyrSerLeuGlnGlnGlnVal 2075
Qy      613 GTTACAAAGGAAAGAAATTTCACTATTAATCACTGAGAGAAATTCAGAACGCTGGCT 672
         |||
Db      2076 ValProArgPheGlnProIleSerGlnHisGlnThrArgGlnValGln-----GlnLeuAla 2094
Qy      673 TCTGGGAAATGAGATGTCACAAAGGTGTGTGAGAAATG-----CGCTATCAGCTG 723
         |||
Db      2095 AsnHisLeuLyrSerLyrThrAspLysCysSerGlnLeuLeuSerLyrSerGlnGlnLeu 2114
Qy      724 AATTAACCAACACTGAGAAAGATGAGGCAAGAAAGAGACAGACAGTTCAGAGCAAA 783
         |||
Db      2115 GlnArgAspIleGlnGlnLyrGlnGln-----GlnIleGlnLyrLeuGlnPheArgValArg 2133
Qy      783 ----- 783
         |||
Db      2134 GlnLeuGlnGlnAlaLeuLeuValSerAlaAspThrPheGlnLyrValGlnAspArgLys 2153
Qy      783 ----- 783
         |||
Db      2154 HisPheGlnValAlaValGlnAlaLysProGlnLyrSerLeuGlnValGlnLeuGlnAlaGln 2173
Qy      784 -----ACTAAC----- 789
         |||
Db      2174 ArgAspAlaIleAspArgLysGlnLyrSerGlnLyrThrAsnLeuGlnGlnGlnGln 2193
Qy      790 -----AGGATCTGAAATTTAAAGATCAGAGAAATGAGAAATGGAATATGATGAT 843
         |||
Db      2194 PheArgGlnLyrLeuGlnLyrLeuLyrSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2213
Qy      844 -----GAAAGCAAAACAACCTTGGAACAGAGACAGACAGAGAGCCCTGGCC 891
         |||
Db      2214 IleGlnLyrSerGlnSerThrThrArgLeuGlnGlnLyrGlnGlnGlnLyrLeuPhe 2233
Qy      892 AGAGAGAGAGCTGAGACTTAACAGAACTGCGCGGAATCTGAG-----CAC 939
         |||
Db      2234 LysAspAspMetGlnLyrSerGlnLyrLeuAlaIleLysGlnSerAspAlaMetSerThrGln 2253
Qy      940 CAATGCACTCACCAGATCTGAATATAGCTCAATGATCAAGCAAAAAAGTATACATAT 999
         |||
Db      2254 AspGlnHisValLeuPheGlnLyrSerPheAlaGlnIleIleGlnLyrSerGlnValGlnIle 2273
Qy      1000 GATTAATTTGGA-----AAGTTACAGAGAA-----AAT 1029
         |||
Db      2274 AspGlnLeuSerGlnGlnValThrLyrSerGlnGlnGlnLyrSerLyrThrThrAspAsn 2293
Qy      1030 GAAGAAATTGAGAA----- 1044
         |||
Db      2294 LysValIleGlnLyrLyrSerGlnLyrLeuLyrLeuArgAspLeuGlnThrGlnIleGlnCysLeu 2313
Qy      1045 -----CAGTGTGTCAGCATGAGGAGTACATGAGACGATGAAGCAAGGCTA 1092
         |||
Db      2314 MetSerAspGlnGlnCysValLysArgAsnArg-----GlnGlnGlnIle 2328
Qy      1093 AGCAGCTGATTAAGACAGCCAGCCACAGCCAGCAGCTGTGACCTCTCAGCAAG 1152
         |||
Db      2329 GlnGlnLeuSerGlnValIleGlnLyrSerGlnGlnGlnGlnLyrLeuLyrSerGlnGlnLys 2348
Qy      1153 CAGAACGACTTCTCTGAGAGAGCAGAGCTGTGGAAGAGGTGAGACCGCTGCGGACC 1212
         |||
```

Db 2349 ThSer-----MetaAlaHisSerLeuSerGluGluAlaSerLeuYHis 2365  
QY 1213 CAGCTTA 1218  
Db 2366 GlnLeu 2367  
RESULT 3  
US-09-949-016-11433  
Sequence 11433 Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL0013107  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11433  
LENGTH: 2733  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-11433  
Alignment Scores:  
Pred. No.: 8.76e-15 Length: 2733  
Score: 253.50 Matches: 119  
Percent Similarity: 40.33% Conservative: 104  
Best Local Similarity: 21.52% Mismatches: 179  
Query Match: 9.28% Indels: 151  
Gaps: 24  
US-09-502-945-1 (1-1552) x US-09-949-016-11433 (1-2733)  
QY 1 CTTCTGGATGCATCCGAGAGCTAAACTTACTTAT-----GAG 39  
Db 1678 ValIleAspGlnuAlaIysIySTpGluArgLySerIleSerAlaIleGlnSerIySGlu 1697  
QY 40 GAAAGCTGAAATTGAGAAATCCCAATTGAAGTTTGAAGAACGACTTGAATAT 99  
Db 1698 GluGluIleArgLeuYSGluAspAenCySerValLeuIyAspGlnLeuArgGlnMec 1717  
QY 100 CAGAGAACTGTGAAGATCTTAA-----GAGCACTAAAGCAT----- 138  
Db 1718 SerIleHisMetGluGluLeuYIleAsnIleSerArgLeuGlnuIleAspLySGlnIle 1737  
QY 139 -----AAGAAATTTCTTGGCTCTAATACTTGTAAACCGTGTGT 180  
Db 1738 TrpGluSerIyAlaGlnThrGluValGlnLeuGlnIyValCyAspThrLeuGln 1757  
QY 181 GGTCTTTGTTGAATGTGCTCAGCATGAAGCTGTTTCCCAACCACTTAAATGTT 240  
Db 1758 Gly-----GluAenIySGluLeuSerGlnLeuGlnIyThrArg 1771  
QY 241 CATATG-----CAGACCATCGAAAGATCGTTTAAAGAAAGATGACTTG 285  
Db 1772 HisLeuYrHisSerSerGlnAenGluLeuAlaLeuGlnIySerGlnLeuYSerLeu 1791  
QY 286 ATGTCTGCACTAGTTTCCGTAAAGAGCAGCTTG----- 318  
Db 1792 LysAspGlnLeuThrAspLeuSerAenSerIleGlnIyScyIySGluGlnIyGlyAsn 1811  
QY 319 -----GCAGATACGACGAAAGAGAGAGCAAGTCTTAT 351  
Db 1812 LeuGlnGlyIleIleArgGlnGlnIyAlaAspIleGlnAenSerIySpheSer---Tyr 1830

QY 352 GAACAGGTGAAACMAATTTTGCATAATCT-----GAGGA 387  
Db 1831 GluGlnLeuGlnuThrAspLeuGlnIleAspArgGluLeuThrSerArgLeuHisGlnGlu 1850  
QY 388 GCCAATTTGAAAAACCAAGCTTTA----- 414  
Db 1851 IleAsnMetIySGlnIyIleIleSerLeuSerGlyIySGluGlnuAlaIleGln 1870  
QY 415 ATCCAGTGTGACGATGTAAGAGAGCGGAGAGCGAGGACGACTTGAAGAAAGAA 474  
Db 1871 ValAlaIleAlaGluLeuArgGlnGlnIleAspLySGluIleYSGluLeuGlnAenLeu 1890  
QY 475 CTTGCATCTCAGCAGAGAAAGAGGCGCATGAGAAAGACATGATGAAAGAAATTAACG 534  
Db 1891 LeuSerGlnGlnIyGlnIyGlnAenIleValLeuGlnGlnIyAsnIySGluValAlaAsp 1910  
QY 535 AAAAGAAAGGATACATGGGATCAAAAGTTTATCTTGTCTCAAAATATGGCCCACTG 594  
Db 1911 LysThrAsnGlnIleuMetGluThrLeuYThrIleYSGluGlnAenIleGlnIy--- 1929  
QY 595 GAGGCCAGGTGAAAGGTTACAAAGAAAGATTTCAAGCTATTAT----- 642  
Db 1930 LysAlaGlnLeuAspSerPheValIySerMetSerIleuGlnAenAspArgAspArg 1949  
QY 643 -----CACTGAGAGAA----- 654  
Db 1950 IleValGlyAspTrpGlnGlnIleuGlnIyArgHisLeuSerIleIleuGlnIyAsp 1969  
QY 655 -----ATTCAAAGCCAGCTGCTTCCGAGAAATGATGTCAAAAGCTGTGAGAA 708  
Db 1970 GlnLeuIleGlnIyAlaAlaIleGluAenIyLeuYSGluIleArgGly--- 1988  
QY 709 ATCGCTATCAGTGAATAAACCACATGCAAGAGATGAGGACAGAAAGGACACAG 768  
Db 1989 LeuArgSerHisMetAspAspLeuAenSerGluAsnAlaIySGlnAspAlaGluLeuIle 2008  
QY 769 GACTTCAGACCAAACTTAACAGGATCTTGAATTAAGAT---CAGGAAATAGAGAA 825  
Db 2009 GlnTrpArgGlnAspLeuAenGlnIleThrIleYAspSerGlnIySGlnIy 2028  
QY 826 TTGAGAAATGAACTGATGAAAGCAAAACA-----CACTTGAAACAG 867  
Db 2029 LeuGlnValGlnIleuGlnIleuGlnIySGluLeuGlnuAsnIyTrpAlaIySGluGln 2048  
QY 868 GAGCAGACAGAGCAGCCCTGCGCAGAGAGAGTCTGAGATTAACAGACCTGCGGC 927  
Db 2049 LysLeuYSGlnSerIyGlnIyAlaenGlnAspLeuArgTrpSerPheAsnAlaLeuGln 2068  
QY 928 GAATCTGAGACCAACTG-----CACTTC 951  
Db 2069 GlnGlnIySGlnAspLeuSerIySGluIleGlnSerLeuYValSerIleSerGlnLeu 2088  
QY 952 ACCAGATCTGAAATGACTCACTCAGTCAAGAA----- 984  
Db 2089 ThrArg---GlnValThrAlaLeuGlnIyGlnIyThrLeuGlnIyLeuYrHisAlaGln 2107  
QY 985 -----AAAAGTATACATGTGAATTTGGGAAAGTTA-----CAGAGA 1023  
Db 2108 LeuYValIySGlnIyGlnIyValHisArgLeuSerAlaLeuYSerSerSerGlnIy 2127  
QY 1024 AGAATGAGAAATTTGAGAGAAACAG-----TGCTGCACAGAT----- 1059  
Db 2128 ArgIleAlaGlnIleuGlnIyGlnIyValCyValGlnIySGluAlaIyIyVal 2147  
QY 1060 GGGAGAGTACATGACGATGAAGCAAGGCTTAAGCAGCTGAT----- 1104  
Db 2148 GlyIyIleGlnIyAspIySGlnIySGluLeuYHisIleuHisIleAspAlaGlyIle 2167  
QY 1105 ---AAGCAGACCAAGGCCACAGCCAGCAGCTGCTG-----CAGCTCTTC 1146  
Db 2168 MetArgAsnIyThrIyThrAlaGlnIyGlnIyValAlaGlnIleuAlaArgAspLeuVal 2187  
QY 1147 AGCAACAGAAACAGCTTCTCTCTG-----GAGAGCCAGAGCTGTGCAAGAGCTG 1197

```
Db      2188 GluMetGluGlnIleuLeuMetValThrIleGluAsnIleuSerGluLeuThrAlaGlnIle 2207
Qy      1198 GACCGGCTGGGACCCAGTATCCAGCATGCAACAATCT 1236
Db      2208 GlnSerPheGlyArgSerMetSerLeuGlnAsnSer 2220

RESULT 4
US-09-949-016-6507
/ Sequence 6507, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: C1001307
/ CURRENT APPLICATION NUMBER: US/09/949, 016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6507
/ LENGTH: 3259
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-6507

Alignment Scores:
Pred. No.:      9,44e-15      Length:      3259
Score:          253.50      Matches:      119
Percent Similarity: 40.33%      Conservative: 104
Best Local Similarity: 21.52%      Mismatches: 179
Query Match:      9.28%      Indels:      151
                        Gaps:      24

US-09-502-945-1 (1-1552) x US-09-949-016-6507 (1-3259)
Qy      1 CTTCTGGATCATCCGAGAACTTAATACTTACTTAT-----GAG 39
Db      2204 ValIleAspGlnIleuLeuSerTrpGluArgLysPheSerAspAlaIleGlnSerIleuGlu 2223
Qy      40 GAAAGGTCGAATTTGAGAAATCCCAATTGAATTTTGGAAACAAGACTTACGTGAATAT 99
Db      2224 GluGlnIleArgLeuLysGlnAspAsnCysSerValLeuLysAspGlnLeuArgGlnMet 2243
Qy      100 CAGAGAACTTGTGAAGATCTTAA-----GAGCACTAAAGCAT----- 138
Db      2244 SerIleHisMetGluGluLeuLysIleAsnIleSerArgLeuGlnIleHisAspLysGlnIle 2263
Qy      139 -----AAAGAAATTTCTTGGCTGCTTAATACTTGAACCGTTGGT 180
Db      2264 TrpGluSerLysAlaGlnThrGluValGlnLeuGlnGlnIleValCysAspThrLeuGln 2283
Qy      181 GGCCTTGTGTTGAAATGTGCTCAGCATGAGACTGTTCTTCCCAACCCACTAATGTT 240
Db      2284 Gly-----GluAsnLysGlnLeuLeuSerGlnLeuGlnIleuGlnIleuThrArg 2297
Qy      241 CATATG-----CAGACCATCGAAAGACTGGTTTAAAGAAAGAGATGACTTG 285
Db      2298 HisLeuTrpHisSerIleArgIleAsnGlnIleuAlaLysLeuGlnSerGlnLeuLysSerLeu 2317
Qy      286 ATCTGCACTAGTATCCGTAAGACAGACTTG----- 318
Db      2318 LysAspGlnLeuThrAspLeuSerAsnSerLeuGlnLysCysLysGlnIleuLysGlnLysAsn 2337
Qy      319 -----GCAGATACGAGCAAAAGAGAGAGAGCAAGCAATGCTTAT 351
Db      2338 LeuGlnGlyIleIleArgGlnGlnIleuAlaAspIleGlnAsnSerLysPheSer--Tyr 2356
```

```
Qy      352 GAACAGTGAACCAAGTTTGCATAATATCT-----GAGGA 387
Db      2357 GluGlnLeuGlnIleuThrAspLeuGlnIleSerArgGluLeuThrSerArgLeuHisGlnIle 2376
Qy      388 GCCAATTTGAAAAAACAAGGCTTAA----- 414
Db      2377 IleAsnMetLysGlnIleuLysIleIleSerLeuSerGlyLysGlnIleAlaIleGln 2396
Qy      415 ATCCAGTGTGACAGTGTGAGAGAGCTGAGAGCGGACGCGGACTTGAAAAAGAA 474
Db      2397 ValAlaIleAlaGluLeuArgGlnGlnIleHisAspLysGlnIleLysGlnLeuGlnAsnLeu 2416
Qy      475 CTTGCATCTCAGCAGAGAAAAAGGCGATTGAGAAAGACATGTGAAAAAGAAATAGCG 534
Db      2417 LeuSerGlnGlnIleuGlnIleuAsnIleValLeuGlnGlnIleuLysLysValAlaAsp 2436
Qy      535 AAAGAAAGGAGATGACATGGGATCAAAAGATGTTGATCTTGTCAAAATTTGCCCAATG 594
Db      2437 LysThrAsnGlnLeuMetGlnIleuLysTrpIleLysLysGlnAsnIleGlnIle 2455
Qy      595 GAGGCCAGGTGGAAAAAGTTTCAAGAAAGATTTCAAGCTATTAT----- 642
Db      2456 LysAlaGlnLeuAspSerPheValLysSerMetSerLeuGlnAsnAspArgAspArg 2475
Qy      643 -----CACTGAGAGAA----- 654
Db      2476 IleValGlyAspTrpGlnGlnIleuGlnIleuArgHisLeuSerIleIleuGlnLysAsp 2495
Qy      655 -----ATTCMAAGCCAGCTGCTTCCGGAATGATGTCAAAAGGTGTGTGAGAA 708
Db      2496 GlnLeuIleGlnIleuAlaIleAlaGluAsnAsnLysLeuLysGlnIleArgGly--- 2514
Qy      709 ATGCGTATCAGTGAATTAACCAATGATGAGAAAGATGAGCAAGAAAGAGACAGAA 768
Db      2515 LeuArgSerHisMetAspAspLeuAsnSerGlnLysAsnAlaLysLeuAspAlaGluLeuIle 2534
Qy      769 GAGTTGAGAGCAAAAATTAACAGGAGCTTGTGAATTTAAAGAT---CAGAAATAGAGAAA 825
Db      2535 GlnTrpArgGlnAspLeuAsnGlnValIleThrIleLysAspSerGlnIleuLysGlnLeu 2554
Qy      826 TTGAGAAATGAACTGATGAAGCAAAACA-----CACTTGGAACAG 867
Db      2555 LeuGlnValGlnLeuGlnIleuLysIleuLysGlnLysLeuLysTrpAlaLysLeuGlnIle 2574
Qy      868 GAGCAGCAGAGGAGCCCTGGCCAGAGAGAGTGCCTGAGACTAACAAGCTGTGGCG 927
Db      2575 LysLeuLysGlnSerGlnIleuAlaAsnGlnLysLeuLysArgSerPheAsnAlaLeuGln 2594
Qy      928 GAATCTGAGCACCAACTG-----CACTTC 951
Db      2595 GluGlnLysGlnAspLeuSerLysGlnIleGluSerLeuLysValSerIleSerGlnLeu 2614
Qy      952 ACCAGATCTGAATAGCTCAACTCAAGAA----- 984
Db      2615 ThrArg---GlnValThrAlaLeuGlnGlnIleuGlnIleuLysLeuGlnLysTrpHisAlaGln 2633
Qy      985 -----AAAGATATCATATGATAATTTGGAAAACTTA-----CAGACA 1023
Db      2634 LeuLysValLysGlnIleuGlnValHisAspGlnSerAlaLeuPheSerSerGlnLys 2653
Qy      1024 AGAATGAGAAATTTGAGAGAACAG-----TGTGTCCACAGT----- 1059
Db      2654 ArgIleAlaGlnLeuGlnIleuGlnIleuValCysValGlnLysGlnLysAlaLysLysVal 2673
Qy      1060 GGGAGAGTACATGAGACATGAAGCAAAAGGCTTAGGACAGCTGAT----- 1104
Db      2674 GlyGlnIleGlnLysLysLysGlnLysGlnLysHisIleuHisHisAspAlaGlyIle 2693
Qy      1105 ---AAGCAGACGAGGCGACAGCCGAGAGCTGGTG-----CAGCTCCGC 1146
Db      2694 MetArgAsnGlnThrGlnThrAlaGlnGlnValAlaGlnLeuAlaAspArgLeuVal 2713
```



```

OY      1147 AGCAAGACGAAACGAGCTTCTCTG-----GAGAGGACGAGCGCTGCGAAGAGGTG 1197
Db      2714 GlnuWctGlnGlnlybLeuWetMetValThrlybGluantylbGlyLeuThralaGlnIle 2733
OY      1198 GACCGGCTCGCGACCCAGTTACCGACGATCGACATCT 1236
Db      2734 GlnserPheGlyArgserMetSerSerIleuInanSer 2746

RESULT 5
US-09-866-108A-15754
; Sequence 15754, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent NO. 6686188
; SEQ ID NO 15754
; LENGTH: 1581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-108A-15754

Alignment Scores:
Pred. No.: 3,14e-14 Length: 1581
Score: 246.50 Matches: 104
Percent Similarity: 41.42% Conservative: 89
Best Local Similarity: 22.32% Mismatches: 172
Query Match: 9.02% Indels: 101
Gaps: 16

US-09-502-945-1 (1-1552) x US-09-866-108A-15754 (1-1581)
OY      16 GAGAACTAAACCTTACTTATGAGAGAAAGCTGTAATTTGAGAAATCCCAATTGAATTT 75
Db      929 LysaIrGleuGInGInGluPheGluAspIysLeuGInValGInGInIaenLyAsrGln 948
OY      76 TTGAGGAACGACTTAGCTGAATATCAGAGACTTGTCAGAGATCTTAA-----GAG 126
Db      949 LeuGInUrGaArgLeuGInYAspLeuGInIlaAspSerGInGInUrGaInArgAlaLeuGln 968
OY      127 CACTTAAGACTTAAAGAAATTTCTTCTGCGCTGCTAAATCTTGAAACCGTTGGTGT-- 183

```

[illegible]



Db 1843 LyeLeu 1844

RESULT 7  
US-09-538-092-1077  
Sequence 1077, Application US/09538092  
Patent No. 6753314  
GENERAL INFORMATION:  
APPLICANT: Glot, Loic  
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
FILE REFERENCE: 15966-542  
CURRENT APPLICATION NUMBER: US/09/538,092  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: 60/127,352  
PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/178,965  
NUMBER OF SEQ ID NOS: 1387  
SOFTWARE: CuraPatSeqFormatter Version 0.9  
SEQ ID NO 1077  
LENGTH: 1960  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (0)-(0)  
OTHER INFORMATION: Polypeptide Accession Number P35579  
US-09-538-092-1077

Alignment Scores:  
Pred. No.: 7,33e-14 Length: 1960  
Score: 243.00 Matches: 106  
Percent Similarity: 40.87% Conservative: 91  
Best Local Similarity: 21.99% Mismatches: 161  
Query Match: 8.89% Indels: 124  
Gaps: 17

US-09-502-945-1 (1-1552) x US-09-538-092-1077 (1-1960)

QY 7 GATGATCCGAGAACTTAATTAAGGAAAG----- 45  
Db 1409 AspLysLeuGlnLysThrLysThrArgLeuGlnGlnLysLeuAspLeuValAsp 1428  
QY 46 -----TTGGAATTGAGGAATCCCAATGAAGTT----- 75  
Db 1429 LeuAspHisGlnArgGlnSerAlaCysAsnLeuGlnLysGlnLysPheAspGln 1448  
QY 76 -----TTGAGGAACGACTTAGTGAATATCAGAGAACTTGTAAGATCTTAA 123  
Db 1449 LeuLeuAlaGlnLysThrLysLeuSerAlaLysLeuLysLeuGlnLysArgAspAlaGln 1468  
QY 124 GAGCACTAAAGCATAAAGATTCTTGGCTGCTAATGTAACCTGTTGGTGGT 183  
Db 1469 AlaGlnAlaArgLysLysGln-----ThyLysAla 1478  
QY 184 CTTTGTGTAATGTGCTCAGCATGAAGCTGTTCTTCCCAACCCATTAATGTTGAT 243  
Db 1479 LeuSerLeuAlaArgLysLeuGlnLysAlaMetGlnLysAlaGln----- 1494  
QY 244 ATGACAGACCTGAAGAAGCTGTTAA-----GAAAGAGTGAATGATGCT 291  
Db 1495 -----LeuGlnLysLeuAsnLysGlnPheArgThrGlnMetGlnAspLeuMetSer 1511  
QY 292 GCACTAGTTCCGTAAGACAGCTTGGACATACGACAAAGAAAGAGCAAGTCTTAT 351  
Db 1512 SerLysAspArgValGlnLysSerValHisGlnLysLysSerLysValAlaLeuGln 1531  
QY 352 GAACAGCTGAACAAGT-----TGCAAAATATCT 381  
Db 1532 GlnGlnValGlnGlnMetLysThrGlnLeuGlnLysLeuGlnLysArgLysGlnAlaThr 1551  
QY 382 GAGGAAGCC-----AATTTGAAAAAACCAAGGCTTAATC----- 417

Db 1552 GluAspAlaLysLeuArgLeuGlnValAsnLeuGlnAlaMetLysAlaGlnPheGlnArg 1571  
QY 418 -----CAGTGTGACCACTTGAAGAGGAGGAGGAGCGG 456  
Db 1572 AspLeuGlnLysArgAspGlnGlnSerGlnLysLysGlnLeuValArgGlnVal 1591  
QY 457 GAGCAGCTTGAAGAAAGCTTGATCTCAGCAAGAGAAAGGCGCATTTGAAAGACATG 516  
Db 1592 ArgGlnMetGlnLysLeuGlnLysLeuAspGlnArgLysGlnArgSerMetAlaValAla 1611  
QY 517 ATGAAAAAGAAATTAAGAAAGAGGAGTACATGGGATCAAAAGTTGATCTGCT 576  
Db 1612 ArgLysLys-----LeuGln 1616  
QY 577 CAGAAATTTGCCCACTGGAGGCCCAAGTGGAAAGATTACAAAGAAAGATTTCAGCT 636  
Db 1617 MetAspLeuLysAspLeuGlnLysAlaHisLeuAspSerAlaAsnLysAsnArgAspGlnAla 1636  
QY 637 ATTAATCACTGAGGAAATTTCAAGCCAGCTG-----GCTTCTGGGAAATGATGTC 690  
Db 1637 IleLysGlnLeuArgLysLeuGlnAlaGlnMetLysAspCysMetArgGlnLeuAspAsp 1656  
QY 691 ACAAGGTGTGAGAGAAATGCGCTATCAGCTGAATPAAACCAAC----- 735  
Db 1657 ThrArgAlaSerArgGlnGlnLysLeuAlaGlnAlaLysGlnLysLysLysLys 1676  
QY 736 -----ATGAGAGAGATGAGCCAGAAAGAGCAGCAGAGAG 771  
Db 1677 SerMetGlnLysLeuMetLysGlnLysGlnLysGlnLysLysLysLysLysLys 1696  
QY 772 TTCAGAGCAAAATTAACAGGAGTCTTGAATTAAGAT----- 810  
Db 1697 ArgGlnHisGlnGlnLysGlnAsp-----GluLeuAlaAspGlnLysLeuAsnSerSerGly 1715  
QY 811 -----CAGGAATAGAGAAATTTAGAAATGAGTGAAGCAAA 852  
Db 1716 LysGlnLysLeuAlaLeuGlnLysLysArgArgLeuGlnLysAlaGlnLysLys 1735  
QY 853 CAACACTTGGACAGAGCAGCAGAAAGGAGCCCTGCCAGAGAGAGTCCAGACTA 912  
Db 1736 GlnGlnLeuGlnLysGlnGlnLysGlnLysGlnLysGlnLysGlnLysGlnLys 1755  
QY 913 ACAGAACTGTGGGCAATCTGAGCAACAATGACCTGACCTGCAATGATGCTCA 972  
Db 1756 AsnLeuGlnLysAspGlnLysLeuThrAspLeuAsnLeuLysSerHis--AlaGln 1774  
QY 973 CTCAGTCAGAAAAAGGTAATACATATGATTAATTTGGAAAGTTACAGAGAAATGAA 1032  
Db 1775 LysAsnGlnAsnHisArgGln-----GlnLeuGlnArgGlnAsnLys 1788  
QY 1033 GAATTTGAGAGACAGTGTCTCCAGCATGGAGAGTACATGACGATGAAGCAAGCTA 1092  
Db 1789 GlnLeuLys-----ValLysLeuGlnGlnLysGlnLysGlnLysSerLysLys 1805  
QY 1093 AGGACAGCTGATTAAGACAGCCAGGACAGCCAGCAGCTGTGACAGCTCTCAGCAAG 1152  
Db 1806 LysAlaSerLysThrLysLeuGlnLysLysLysLeuGlnLysGlnLysLeuAspAsn 1825  
QY 1153 CAGAACCACTTCTCTGAGGAGCAGAGCTGTGCGAAAGGTGACCGGCTCGGAGCC 1212  
Db 1826 GluThrLys-----GluArgGlnAlaAlaCysLysGlnValArgArgThrGlnLys 1842  
QY 1213 CAGCTTA 1218  
Db 1843 LysLeu 1844

RESULT 8  
US-09-538-092-1252  
Sequence 1252, Application US/09538092  
Patent No. 6753314  
GENERAL INFORMATION:  
APPLICANT: Glot, Loic

```

; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurataseqFormatter Version 0.9
; SEQ ID NO: 1252
; LENGTH: 2663
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q02224
; US-09-538-092-1252

```

```

Alignment Scores:
Pred. No.: 1 04e-13 Length: 2663
Score: 242.00 Matches: 112
Percent Similarity: 43.45% Conservative: 97
Best Local Similarity: 23.28% Mismatches: 162
Query Match: 8.86% Indels: 110
Gaps: 22

```

```
US-09-502-945-1 (1-1552) x US-09-538-092-1252 (1-2663)
```

```

QY 1 CTTCTGATGATCCAGAGCTAAACCTTACTTATGAGAAAGCTGAAATGAGAA 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 722 lIethrAspleuInlysgluLeuAnlysgluValgluIngluAnlygluVal 741
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 -----TCCCAATGAGTTTGGAGAACCTAGCTGAATTCAGAGA 105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 742 gluValIleleuLeuSerleuLeuLysSerleuProserIuValgluArgleuArglys 761
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 106 ACTTGAGAGATCTTAAAGCAACTA-----AAGCATAAAGATT 147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 762 gluIleInleuSerleuInleuHleIleIleThSerleuLysAspLysleuPhe 781
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 148 CTTCTGCTGCTAATCTGTAAACGCTGTGTGCTTTGTTGAATGCTCAGCAT 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 782 SerIuValIleHleLysgluSerArgValgluIngluLeuIngluInleuLysThr 801
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 208 GAAGCTGTTCTTCCAAACCCACTACTAAT----- 237
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 802 LysAspAspLeuAlaThrThrInSerAsnTyLysSerThrAspIngluPheInAsn 821
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 -----GTTCAATG----- 246
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 822 PheLysThrleuHleSheAspPheIngluInlyTyLysMetValleuIngluInAsn 841
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 247 -----CAGACATCGAAGAGCTGTTAAAGAAAGAGATGATGATGCTGACTA 297
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 842 ArgMetAsnIngluInleuValAsnLeuSerlygluInlySphaeAspSerleu 861
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 298 GTTCCGTAAGCAGCTTGGA-----GATACGACGAAGAAAGCAAGT 345
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 862 GlyAlaLeuLysThrIleuSerTyLysThrIleuIngluInlySphaeAspSer 881
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 346 GCTTATGACAGGTAACAGGTTTGCAATATCTGAGGA----- 387
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 882 ValIngluInlyLeuIngluMetGluInleuLysgluInleuIngluAsnArgAspSer 901
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 388 -----GCCAATTTAAACCAAGGCTTATCATCAGTGTGACAGTGGAGAGAG 441
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 902 ProleuInThrValgluArgLysThrleuIle---ThrIlySleuIngluInThr 920
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 442 CTGGAGGCGAGCGGAGCGACTTGAAGAAAGAA-----CTTGATCTCAGCAAGAG 492
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

Db 921 LeuGlu---GluValLysThrleuThrIngluInlyAspAspLeuLysgluInglu 939
QY 493 AAAAGGCCATTGAGAAAGACATGATGAAAGAAATTAACGAAAGAGAGTACATG 552
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 940 SerleuGluInleuLysArgPheInleuLysSerArgPheIleHleAsp----- 954
QY 553 GGATCAAGATGTTGCTTCTGCTCAGATATT-----GCCCACTGAGGCCAG 603
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 955 -----ThrValAsnMetAsnIleAspThrIngluInleuInlyArgAsnAla 969
QY 604 GTGGAAAGATTACAAGAAAGAAAGATTGAGCTATTATCACTGAGGAAATTCAGAG 663
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 970 LeuGluSerleu---LysgluInleuInlyThrIleAsnThrleuLysSerlyIleSer 988
QY 664 CAGCTGCTTCTCGGAAATGATGATCAGAAAGTGTGTGAGAAATGCGC-----TAT 717
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 989 GluIngluValSerArgAsnleuHleMetGluInleuAsnThrGlyInlyThrLysAspLysPhe 1008
QY 718 CAGCTGAATTAACCAATGAGAAAGATGAGGCGAAAGAGACAGAGATTTCAGA 777
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1009 GluIngluLysMetValGlyIleAspLysLysgluIn-----AspLeuGlu 1022
QY 778 GCAAAACATTAACAGGATCTT-----GAAATTAAGATCAGGAATA-----GAG 822
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1023 AlaLysAsnThrGluInlyThrIleAspValLysAspAsnInleuIleleuIngluIn 1042
QY 823 AATTTGAGATGAATGATGATGATGAAAGCAAACTTGGAAACAGAGACAGCAAGAGCA 882
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1043 ArgLysIlePheSerleuIleIngluInlySAsnIngluLeu---GluInleuLeuGluSer 1061
QY 883 GCCCTGCGCAGAGAGAGTGCCTGAGACTA-----ACAGAACTGCTGGGC 927
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1062 ValIleAlaGluLysgluInleuLysThrAspLeuLysgluAsnIleleuMetThrIle 1081
QY 928 GAATCGACACCAATGACACCTCACCAGATCTGAATAGCTCA-----CTC 975
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1082 GluAsnIngluInleuLysgluInleuLysAspGluInleuLysgluIngluIleVal 1101
QY 976 AGTCAAGAAAGAAAGATGATCATATGATTAATTTGGAAAGTTACAGAGAAATGAAGAA 1035
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1102 AlaIngluInlyAsnHleAlaIleLysLysgluIngluLysSerArgThrCysAspArg 1121
QY 1036 TTGGAGAAACAGTGTCTCAGCATGGGAGAGATACATGAGACATGAAGCAAGAGCTAAG 1095
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1122 LeuAlaGlu-----ValGluIngluLysleuLysgluLysSerGln 1134
QY 1096 CAGCTGATTAAGACAGCGCAGGCGACAGCCAGCAGCTGATGAGCTCCAGCAAGCAG 1155
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1135 GluLeuGluInlySgluIn-----GluLeuLeuAsnValGln 1147
QY 1156 AACCACTTCTCCTGAGAGAGCAGAGCTGTGCGAAGAGGTGAGCCGCTGCGAGCCAG 1215
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1148 GluGlu---MetSerLysMetGluInlyLysIleAsnGluInleuLysAsnGlu 1166
QY 1216 TTA 1218
   ||| |||
Db 1167 Leu 1167

```

# RESULT 9

```

US-09-538-092-1078
; Sequence 1078, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01

```



Score: 239.50 Matches: 111  
Percent similarity: 43.45% Conservative: 98  
Best Local Similarity: 23.08% Mismatches: 161  
Query Match: 8.77% Indels: 111  
DB: 4 Gaps: 22

US-09-502-945-1 (1-1552) x US-09-595-684B-31 (1-2662)

```

QY 1 CTTCTGATCCATCCGAGAGCTAAACTTACTTATGAGAAAGTGTGAATTTGAGAA 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 722 lIeThraPlenGlnlyserGluLeuAenlyGluValGlnGluAenGlnlaleuAArglu 741
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 -----TCCCAATTGAAGTTTGAAGAACGACTTACGTGAATTCAGAGA 105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 742 GluValIleuLeuSerGluLeuLySerLeuProSerGluValGluArgLeuArglys 761
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 106 ACTTGAGAGATCTTAAAGCAACTA-----AAGCTAAAGAAATT 147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 762 GluIleGlnMetPysSerGluLeuHisIleIleThSerGluPysApIysLeuPhe 781
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 148 CTTCTGCTCTTAATCTGTAAACGTTGTGTGCTTTGTTGAAATGCTCAGCAT 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 782 SerGluValValHisIlySerArgValGlnGlyLeuLeuGlnGluIleGlyPThr 801
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 208 GAAGCTGTTCTTCCCAACCCACTACTAAT----- 237
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 802 LysAspAspLeuIleThrThrGlnSerAsnTyIysSerThrAspGlnGluPheGlnAsn 821
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 -----GTTCAATATG----- 246
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 822 PheLyThrLeuHisMetAspPheGlnGlyIleTyIysMetValleuGlnGluAenGlu 841
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 247 -----CAGACCATCGAAGAGCTGTTAAAGAAAGAGATGATGATCTGCACTA 297
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 842 ArgMetAsnGlnIleValleuLeuSerLyGlnGlnGlnPheAspSerSerLeu 861
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 298 GTTTCGTTAAGAGCAGCTTGCA-----GATACGACGAAAGAGACAGT 345
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 862 GlyAlaLeuLyThrGlnLeuSerTyIysThrGlnGlnGlnGlnGlnGlnGln 881
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 346 GCTTATGACAGGTGAACAAGTTTGCAATATCTGAGAA----- 387
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 882 ValGlnGlnArgLeuAsnGlnMetGlnGlnLeuLySerGlnGlnGlnGlnGlnGlnGln 901
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 388 -----GCCAATTGTGAACCAAGGCTTATCCAGTGCAGGAGTGAAGAGAG 441
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 902 ProLeuGlnThrValGlnArgGlyPThrLeuIle-----ThrGlnPysLeuGlnGlnThr 920
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 442 CTGAGAGCAGCAGCAGCAGCTTGAAGAA-----CTTGCAATCTCAGCAAG 492
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 921 LeuGlu-----GluValIlyThrLeuThrGlnGlnIlySerAspLeuLySerGlnGlnGln 939
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 493 AAAAGGGCCATTGAAGAACGATGAAGAAAGAAATACGAAGAAAGAGAGTACATG 552
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 940 SerLeuGlnIleGlnArgAspGlnLeuLySerAspIleHisAsp----- 954
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 553 GGATCAAGATGTTATCTTCTCTCAGAAATATT-----GCCCAACTGAGGCCAG 603
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 955 -----ThrValAsnMetAsnIleAspThrGlnGlnGlnGlnGlnGlnGlnGlnGln 969
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 604 GTGGAAGAGGTTACAAAGAAAGATTTACGTTATTAATCACTGAGAGAAATCAAGC 663
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 970 LeuGlnSerLeuLyHisGlnGln-----ThrIleAsnThrLeuLySerLyIleSer 987
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 664 CAGCTGGCTCTCGGAAATGATGTCAACAAAGTGTGTGGAATAATGGCC-----TAT 717
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 988 GluGlnValSerArgAsnLeuHisMetGlnGlnAsnThrIlyGlnThrIlyAspGluPhe 1007
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 718 CAGCTGAATTAACCAACAGAGAGATGAGCAGAGAAAGAGACAGAGATTTCAGA 777
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1008 GlnGlnIlyMetValGlnIleAspLyIlySerGln-----AspLeuGln 1021
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 778 GCAAAAACTTAACGAGCATCTT-----GAAATTAAAGATCAGAAATA-----GAG 822

```

```

Db 1022 AlaIysAsnThrGlnThrLeuThrAlaAspValIysAspAsnGlnIleIleGlnGln 1041
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 823 AAATTGAGATGAAGATGATGAAGAAACAAACCTTGAAACAGAGCAGCAGAGAGCA 882
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1042 ArgLyIlePheSerLeuIleGlnGlnPysAsnGlnLeu-----GlnGlnMetLeuGlnSer 1060
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 883 GCCCTGGCAGAGAGAGTGCCTGAGACTA-----ACAGAACTGCTGGC 927
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1061 ValIleAlaGlnIlySerGlnLeuLySerThrAspLeuLyGlnAsnIleGlnMetThrIle 1080
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 928 GAATCTGACACCAACTGCACCTCACCAGATCTGAATAGCTCA-----CTC 975
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1081 GluAsnGlnGlnGlnLeuArgLeuGlnIlyAspGlnLeuLySerGlnGlnGlnGlnIleVal 1100
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 976 AGTCAAGAAAGATATCATATGATTAATTGGGAAATTCAGAGAAATGAAGAA 1035
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1101 AlaGlnGlnIlyAsnHisAlaIleLySerGlnGlnGlnLeuSerArgThrCysAspArg 1120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1036 TTGAGAGAACGTGTCTCAGCATGGAGAGTACATGACATGACATGAAGCAAGCTTAAG 1095
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1121 LeuAlaGln-----ValGlnGlnIlyLeuLySerGln 1133
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1096 CAGCTGGATTAAGACAGCAGCCACAGCCACAGCTGTGAGCTCTCAGCAAGCAG 1155
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1134 GlnLeuGlnGlnIlySerGln-----GlnLeuLeuAsnValGln 1146
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1156 AACCAAGCTTCTCTGAGAGAGAGAGCTGTGCAAGAGTGAACCGCTGCGAGACCCAG 1215
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1147 GluGln-----MetSerGlnMetGlnIlySerIleAsnGlnIleGlnAsnLeuLySerGln 1165
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1216 TTA 1218
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1166 Leu 1166

```

RESULT 11

US-09-866-108A-15753

/ Sequence 15753, Application US/09866108A

/ Patent No. 6686188

/ GENERAL INFORMATION:

/ APPLICANT: GU, Yizhong

/ APPLICANT: JI, Yonggang

/ APPLICANT: PENN, Sharron G.

/ APPLICANT: HANZEL, David K.

/ APPLICANT: RANK, David R.

/ APPLICANT: CHEN, Wensheng

/ APPLICANT: SHANNON, Mark

/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

/ FILE REFERENCE: AEOMICA-7

/ CURRENT APPLICATION NUMBER: US/09/866, 108A

/ PRIOR FILING DATE: 2001-05-25

/ PRIOR APPLICATION NUMBER: US 60/207, 456

/ PRIOR FILING DATE: 2000-05-26

/ PRIOR APPLICATION NUMBER: GB 24263.6

/ PRIOR FILING DATE: 2000-10-04

/ PRIOR APPLICATION NUMBER: US 60/236, 359

/ PRIOR FILING DATE: 2000-09-27

/ PRIOR APPLICATION NUMBER: PCT/US01/00666

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00667

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00664

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00669

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00665

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00668

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00663

/ PRIOR FILING DATE: 2001-01-30

/ Remaining Prior Application data removed - See File wrapper or PALM.

/ NUMBER OF SEQ ID NOS: 15755





```

Db      1057 AspglnAsnArgLeuLysGlnIleLysAsnGlnIleAspSerLeuLysGln 1076
QY      97  TATCAAGAAAGCTTGTGAAGATCTTAAAGACAACTAAAGCATTAATTTCTTGAGCT 156
Db      1077 LysGlnThrLeuIleGlnGlnLeuLysGlnGlnLeuGlnIleLysAsnValThrLeuAsp 1096
QY      157  GCTAATATCTTGAACCGCTGTGGTGTG-----CTTTGTTGAAATGT 198
Db      1097 ValGlnIleGlnIleValIleGlnIleLysArgAlaLeuSerGlnLeuThrGlnIleVal 1116
QY      199  GCTCAGCATGAAAGCTGCTTCTTCCCAACCATATGTTATGTTATATGACAGCATGCA 258
Db      1117 ThrCysThrLysAlaLysIleLysGlnLeuGlnThrIleLeuGlnThrGlnLysValGln 1136
QY      259  AGA-----CTGCCTTAAGAAAGAGATGACTGATG-----TCGTCACTAGTTTCC 303
Db      1137 ArgSerHisSerLysIleLysLeuGlnIleAspIleLeuGlnLysGlnSerIleIleLeuLys 1156
QY      304  GTAAGAGACAGCTTGGCAGATACGACGAAAGAAAGAAAGCAAGTCTTAAGAACAGTGA 363
Db      1157 LeuGlnLysArgAsnLeuLysGlnPheGlnGlnIleLeuGlnIleAspSerValLysAsnThrLys 1176
QY      364  CAAGTT-----TTGCAAAATATCTGAGGAAGCC-----AATTTT 396
Db      1177 AspLeuAsnValLysGlnLeuLysLeuLysGlnGlnIleThrGlnLeuThrAsnAsnLeu 1196
QY      397  GAAAAAACAAGCACTTATATCCAGTGTGACCAAGTGTGAGAGAGCTGAGAGAG----- 453
Db      1197 GlnAspMetLysIleLysLeuGlnLeuLysGlnGlnIleGlnIleGlnIleGlnIleGlnIle 1216
QY      454  GCGGAGCGACTTGAAGAAAGACTT--GCATCTCAGCAGAAAGAAAGCGCCATTGAGAAA 510
Db      1217 ThrGlnLysLeuLysGlnGlnIleLysSerAlaSerSerAlaArgThrGlnAsnLeuVal 1236
QY      511  GACATGATGAAAAAGAAATTAAGAAAGAAAGAGATGATGAGTGAAGATGTTGATC 570
Db      1237 AspLeuGlnArg-----LysGlnGlnAspLysLysLys----- 1247
QY      571  TTGTCTCAGAAATATGTCGCCAATGAGAGCGCCAGGTGAGAAAGCTTAAAGAAAGAT 630
Db      1248 LeuLysGlnLysLeuThrAspAlaLysLysGlnIleLysGlnValGlnLysGln--Val 1266
QY      631  TCAGCT-----ATTATCAACTGAGGAAAT 657
Db      1267 SerValMetArgAspGlnAspLysLeuLysArgIleLysIleAsnGlnLeuGlnLys 1286
QY      658  CAAAGCAGCTGCTTCTCGGAAATGATGTC--ACAAGGTGTGTGAGAAATGCC 714
Db      1287 LysAsnGln--CysSerGlnGlnLeuAspMetLysGlnArgThrIleGlnGlnLys 1305
QY      715  TATCAGCTGAAATTAACCAATGAGAGAGATGAGAGAAAGAGAGACACAGAGATTG 774
Db      1306 GlnGlnLeuAsn-----AsnGlnLysValGlnIleGlnIleGlnIleGlnIleGlnIle 1321
QY      775  AGAGCAAAAACTAACAGGATCTTGAATTAAGATCAAGAAATTAAGAAATTAAGAAATA 834
Db      1322  -----ArgLysCysLysAspLeuAsnValLysGlnLysIleIleGlnAspMetArgMet 1339
QY      835  GAATGATGAAAGCAAAACAACCTTGAGACAGAGACAGAGAGAGAGAGAGAGAGAG 894
Db      1340 ThrLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1359
QY      895  GAGAGAGCTGAGCACTA--ACAGAACTGCTGGCGAATCTGAGACCAACAGCACTG 951
Db      1360 GlnGlnValGlnLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLys 1379
QY      952  ACCAGATCTGAATTAAGCTCAACTCAGTCAAGAAAGAAAGAGTATCATATGATTAAT 1011
Db      1380 GlnThrLysAsnAsnIleArgSerAsnLysGlnIleGlnLysAsnThrAspValLeuGln 1399
QY      1012  AACTTACAGAGAAATGAAGAA----- 1035

```

```

Db      1400 LysLeuThrAsnLeuGlnAspGlnLeuGlnGlnSerGlnGlnLysThrAsnAlaAspArg 1419
QY      1036  -----TTGAGAGAACAGTGTGTCCAGCATGGAGAGTACATGAGACGATGAAGCAA 1086
Db      1420 LysLysThrLeuGlnGlnLysMetMetLeuIleThrGlnAlaLysGlnIleGlnIle 1439
QY      1087  AGGCTTAAGCAGCTGATTAAGACAGC-----CAGGCCACA 1122
Db      1440 ArgAsnLysGlnMetLysLysThrLysArgLysAspArgLysArgPhePheLysGlnGln 1459
QY      1123  GCCCAGCAGCTGGTG-----CAGTCTCTCAGACAGACAGACAGCTTCTCTGAGAGG 1176
Db      1460 GlnMetGlnIleLeuThrAlaGlnLeuThrGlnLysAspSerAspLeuGlnLysThrArg 1479
QY      1177  CAGAGCCTGTGAGAGAGTGAACCGCTGCGGACCCAGTTAACCATGCCACAATCT 1236
Db      1480 GlnGlnLysArgAspGlnLeuValAlaAlaLeuGlnIleGlnLeuLysAlaLeuIleSer 1499
QY      1237  GAT 1239
Db      1500  Asn 1500

```

## RESULT 13

```

US-09-949-016-7880
/ Sequence 7880, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OR INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7880
/ LENGTH: 1786
/ TYPE: PRT
/ ORGANISM: Human
/ US-09-949-016-7880

```

## Alignment Scores:

```

Pred. No.: 1,86e-13 Length: 1786
Score: 238.50 Matches: 108
Percent Similarity: 44.47% Conservative: 97
Best Local Similarity: 23.43% Mismatches: 179
Query Match: 8.73% Indels: 77
DB: 4 Gaps: 19

```

US-09-502-945-1 (1-1552) x US-09-949-016-7880 (1-1786)

```

QY      37  GAGGAAAGGTGTAATTAAGATGCAATGGAATTTTGAAGACGATTAAGCTGA 96
Db      1063  AspglnAsnAsnArgLeuLysGlnIleLysAsnGlnIleAspSerLeuLysGln 1082
QY      97  TATCAGAAAGCTTGTGAAGATCTTAAAGACCACTAAAGCATTAAGAAATTTCTTG 156
Db      1083  LysGlnThrLeuIleGlnGlnLeuLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1102
QY      157  GCTAATATCTTGAACCGTGTGGTGTG-----CTTTGTTGAAATGT 198
Db      1103  ValGlnIleGlnIleValIleGlnIleLysArgAlaLeuSerGlnLeuThrGlnIleVal 1122
QY      199  GCTCAGCATGAAAGCTTCTTCCCAACCATATGTTATGTTATATGACAGCATGCA 258
Db      1123  ThrCysThrLysAlaLysIleLysGlnLeuGlnThrIleLeuGlnThrGlnLysValGln 1142

```

QY	259	AGA-----CTGGTAAAGAAAGATGACTTGATG-----TCGCACTAGTTC	303
Db	1143	ATGserHisSerAlaLysLeuGluGlnAspIleLeuGluLysGluSerIleLeuLys	1162
QY	304	GTAAGAGACACTTGGCAGATACCGAGCAAGAGAAAGCAAGTGCCTTAAGAACAGGTGAA	363
Db	1163	LeuGluATGAnLeuLeuGluPheGlnGlnIleuGlnAspSerValLysAsnThrLys	1182
QY	364	CAAGT-----TTGCATAATCTGAGGAGCC-----AATTTT	396
Db	1183	AspLeuAsnValLysGluLeuLysLeuLysGluGlnIleThrGlnLeuThrAsnAsnLeu	1202
QY	397	GAAGAAACCAAGGCTTTAATCCAGTGTACCAAGTCAGAGAAAGAGCTGAGAGGAG---	453
Db	1203	GlnAspMetLysVHLeuLeuGlnIleuLysGluGlnGluGlnIleuThrAsnArgIleGlu	1222
QY	454	GCGGAGCAGCTTGAAAGAAAGAACTT---GCATCTCGCAAGAGAAAGGCGCATTGAGAA	510
Db	1223	ThrGluLysLeuLysGluGlnLeuSerIleAsnSerAlaArgThrGlnAsnLeuVala	1244
QY	511	GACATGATGAAAAAGAAATACGAAAGAAAGGAGTACATGGATCAAGAATGTGATC	570
Db	1243	AspLeuGlnArg-----LysGluGlnAspTyrAlaAsp-----	1253
QY	571	TTGTCTCAGAAATATTGCCCACTGGAGGCCCGAGGTGGAAAGGTTACAAAGAAAGTT	630
Db	1254	LeuLysArgIleLysLeuThrAspAlaLysLysGlnIleLysGlnValGlnLysGlu---Val	1272
QY	631	TCAGCT-----ATTAACTCACTGAGGAATT	657
Db	1273	SerValMetArgAspGluAspLysLeuLeuArgIleLysIleAsnGluLeuGluLysLys	1293
QY	658	CAAGCCAGCTGGCTTCTCGGAAATGAGATGC--ACAAAGCTGTGTGAGAAATGGC	714
Db	1293	LysAsnGln---CysSerGlnGlnLeuAspMetLysGlnArgThrIleGlnGlnLeuLys	1311
QY	715	TATCAGCTGAAATMAACCAACATGGAGAAAGATGAGCGAGAAAGAGCACAGAGATTC	774
Db	1312	GluGlnLeuAsn-----AsnGlnLysValGluGlnValaIleGlnGlnTyrGln-----	1327
QY	775	AGAGCAAAACCTAACAGGATCTTGAATTTAAAGTCAGAAATAGAGAAATTGAGATTA	834
Db	1328	-----ArgAlaCysLysAspLeuAsnAlaLysGluLysIleIleGluAspMetArgPheC	1345
QY	835	GAATGTGATGAAAGCAACCACTTGGACAGAGCAGCAGAAAGGCAAGCCCTGGCCAGA	894
Db	1346	ThrLeuGlnGluGlnGlnGlnIleThrGlnValaGluGlnAspGlnValaLeuGlnAlaLysLeu	1365
QY	895	GAGAGATGCTCGAGACTA--ACAGAACTGCTGGCGAATGTGAGACCAACTGCACCTC	951
Db	1366	GluGlnValaGluArgLeuAlaThrGluLeuGlnLysTyrPlyGlnLysCysAsnAspLeu	1385
QY	952	ACCAAGATCTGAATAGCTCAACTCAGTGCAGAAAAAAGCTATACATAGATTAATTGGGA	1011
Db	1386	GluThrLysAsnAsnGlnArgSerAsnLysGlnIleGluAsnAsnThrAspValLeuGly	1405
QY	1012	AAGTTACAGAGAAAGAAATGAAGAA-----	1039
Db	1406	LysLeuThrAsnLeuGlnAspGluLeuGlnGlnIleuSerGluGlnLysTyrAsnAlaAspArg	1425
QY	1036	-----TTGAGAGAAACAGTGTGTCCAGCATGGAGAGAGTACATGAGACATGAAGCAA	1086
Db	1426	LysLysTyrPheLysGluGlnLysMetMetLeuIleThrGlnAlaLysGluValaGluAsnIle	1445
QY	1087	AGGCTAAGGCAAGCTGGAATTAACACAGC-----CAGGCCACA	1122
Db	1446	ArgAsnLysGluMetLysLysTyrAlaGluAspArgLysArgPheLysGlnGlnAsn	1465
QY	1123	GCCCGCAGCTGAGT-----CAGCTCTCAGACAGCAAGCAAGCTTCTCTGGAGAG	1176
Db	1466	GluMetGluIleLeuThrAlaGlnLeuThrGluLysAspSerAspLeuGlnLysTyrArg	1485
QY	1177	CAGAGCTGTGGAAGAGGTGAGCCGGCTGGAGACCCAGTTAACCCAGATGCGACAAATCT	1236

Db	1486	GlutGluArgAspGlnLeuValAlaAlaLeuGluIleGlnLeuLysAlaLeuIleSer	1505
QY	1237	GAT 1239	
Db	1506	Asn 1506	
RESULT 14			
US-09-949-016-9776			
Sequence 9776, Application US/09949016			
Patent No. 6812339			
GENERAL INFORMATION:			
APPLICANT: VENTNER, J. Craig et al.			
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED			
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF			
FILE REFERENCE: C1001307			
CURRENT APPLICATION NUMBER: US/09/949, 016			
PRIORITY FILING DATE: 2000-04-14			
PRIORITY APPLICATION NUMBER: 60/241,755			
PRIORITY FILING DATE: 2000-10-20			
PRIORITY APPLICATION NUMBER: 60/237,768			
PRIORITY FILING DATE: 2000-10-03			
PRIORITY APPLICATION NUMBER: 60/231,498			
PRIORITY FILING DATE: 2000-09-08			
NUMBER OF SEQ ID NOS: 207012			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 9776			
LENGTH: 1055			
TYPE: PR			
ORGANISM: Human			
US-09-949-016-9776			
Alignment Scores:			
Pred. No.: 2.06e-13			
Score: 237.00			
Percent Similarity: 43.86%			
Best Local Similarity: 22.27%			
Query Match: 8.67%			
DB: 4			
US-09-502-945-1 (1-1552) x US-09-949-016-9776 (1-1055)			
QY	4	CTGATGATCCCGAGAACTTAACTTATGAGAAAGTGGAAATTGAGCAATCC	63
Db	533	LeuLagIntHrlyArgValLeuAlaAlaLagIntHrlySerLysMetGlnGlnSer	552
QY	64	CAATTGAAGTTTGGAGAGCACTAGCTGATATGAGAGAACTTGTGAAGATCTT	120
Db	553	AsnLeuGluLysLeuGluLeuAlaValArgLysLeuGlnGlnLeuAspGlnLeuAla	572
QY	121	-----AAAGCACTAAAGCATATA	141
Db	573	ArgAspLysLeuSerLeuHisAsnAspLLeSerAlaMetGlnGlnLeuGlnLys	592
QY	142	GAATTTCTTGTGCTGCTAATGCTTGTGAACCGTGTGCTTGTGTTGTAATGCT	201
Db	593	Arg-----GluAlaValAsnSer-----Leu	599
QY	202	CAGCATGAAGCTGTTCTTCCCAACCCATCTAATGTCATATGACAGACATCGAAGA	261
Db	600	GlnGlnGluLeuAlaValGlnAspLysLeuAlaLysGlnAspLeuLeuHis	619
QY	262	CTGGTTAAAGAAAGATGACTTGTATGCTGCTACATGTTCCGTAAGAGCAGCTTGCA	321
Db	620	ThrThrLysHisGlnAspValLeuLeuSerGlnGlnThrArgLysGlnLysAspLLeSer	639
QY	322	GATTCGCGAG-----CAAGAGAAAGCAAGTGTCTTAATGACAGAGTGA	363
Db	640	GluTrpAlaAsnArgPheGluAspCysGlnLysGlnGlnGlnThrLysGlnGlnGlnLeu	659
QY	364	CAAGTTTTCGAATATATGAGGAAGCAATTTTGAATAAACAAGAGCTTAACTCCAGT	423
Db	660	GlnValLeuGlnAsnGlnLLeGlnGlnSer-----LysLeuLys--LeuValGlnGln	676



```
QY 685 GATGTCAAAAGGTGTGTGGAGAAATGCGCTATCAGCTGAATATAAACCAATGAGAGAG 744
Db 1133 -----AlaLysAlaGluLysGlnArgSerAspLeuSerArgGluLeu 1146
QY 745 GATGAGCGAGAAAGAGACAGAGAGTTCAAGCAAAAATAAGAGGATCTTGAATAT 804
Db 1147 GlnGluLysSerGlnArgLeuGlnGluAlaGlyValAlaThrSerAlaGlnValGluLeu 1166
QY 805 -----AAAGATCAGAAATATAGAAATGAGAAATAGACTGAGTGAAGCAAAACAA 855
Db 1167 AsnLysLysArgGluAlaGlnPheGlnLysLeuArgAspLeuGlnGluAlaThr-- 1185
QY 856 CACTTGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 915
Db 1186 --LeuGlnHisGlnLysMetValAlaAlaLeuArgLysHisAlaAspSerMetAla 1204
QY 916 GAACTGCTGGGCGAATCTGAGACCAATGCACTCACCAGATCTGAATAGCTCAATC 975
Db 1205 Glu--LeuGlyGlnGlnLysAspAsnLeuGlnArgValLysGlnLysLeuGlnLysGlu 1223
QY 976 AGTCAAGAAAAAGTATACATATGATTAATTG----- 1008
Db 1224 LysSerGlnLeuLysMetGlnThrAspAspLeuSerSerAsnAlaGlnAlaLysSerLys 1243
QY 1009 -----GAAAGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1062
Db 1244 AlaLysGlnLysAsnLeuGlnLysMetCysArgSerLeuGlnAspGln--ValSerGlnLeu 1262
QY 1063 AGAGTACATGAGACGATGAAGCAAGGCTA----- 1092
Db 1263 LysThrLysGlnGlnGlnGlnGlnGlnGlnLysAsnAspLeuThrAlaGlnArgAlaArg 1282
QY 1093 -----AGGCAGCTGAT----- 1104
Db 1283 LeuGlnThrGlnLysGlnGlnLysArgGlnLeuAspGlnLysAspAlaLeuValSer 1302
QY 1105 -----AAGCAGAGCCAGAGCCAGAGCCAGAGCTGTCAGAGCTC----- 1143
Db 1303 GlnLeuSerArgSerLysGlnAlaSerThrGlnGlnLysGlnLysLeuLysHisGlnLeu 1322
QY 1144 -----CTCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1194
Db 1323 GluGlnGlnLysThrLysAlaLysAsnAlaLeuAlaHisAlaLeuGlnSerSerArgHisAsp 1342
QY 1195 GTGAGACCGGCTGGGAGCCAG 1215
Db 1343 CysAspLeuLeuArgGlnGln 1349
```

Search completed: March 12, 2005, 00:41:29  
Job time : 106.912 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 12, 2005, 00:25:19 ; Search time 68.6159 Seconds

(without alignments)  
6277.336 Million cell updates/sec

Title: US-09-502-945-2

Perfect score: 5346  
Sequence: 1 ggaattcccttgcgaagt.....aaacaaagtaaaattc 2885

## Scoring table:

Xgapop 10.0 ,	Xgapext 0.5
Ygapop 10.0 ,	Ygapext 0.5
Fgapop 6.0 ,	Fgapext 7.0
Delop 6.0 ,	Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

-MODE=frame+n2p-model -DEV=x1p  
-Q=/cgn2\_1/USPTO.spool\_p/US09502945/runat\_10032005\_164737\_13306/app\_query.fasta\_1.10979  
-DB=Issued\_Patents\_AA -OPMT=faetan -SUFFIX=mar9.ra1 -MINMATCH=0.1 -LOOPL=0  
-LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blonum62 -TRANS=human40.cdd  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09502945 -OCGN\_1\_1\_283 @runat\_10032005\_164737\_13306 -NCPUS=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4677	87.5	897	4	US-09-849-602-18
2	4560.5	85.3	1114	4	US-09-637-145-4
3	2691	50.3	1041	4	US-09-644-827B-9
4	2691	50.3	1084	4	US-09-637-145-3
5	2691	50.3	1084	4	US-09-538-092-1222
6	1773	33.2	938	4	US-09-637-145-2
7	1739.5	32.5	1200	4	US-09-644-827B-8
8	1739.5	32.5	1428	4	US-09-644-827B-7
9	1573	29.4	574	4	US-09-644-827B-6
10	672	12.6	706	4	US-09-538-092-649
11	562.5	10.5	527	4	US-09-270-767-45990
12	515	9.6	341	4	US-09-902-540-15627

13	477.5	8.9	386	4	US-09-248-796A-15279	Sequence 15279, A
14	464.5	8.7	141	4	US-09-270-767-33310	Sequence 33310, A
15	447	8.4	630	4	US-09-252-991A-18033	Sequence 18033, A
16	409.5	7.7	387	4	US-09-489-039A-12997	Sequence 12997, A
17	374.5	7.0	335	3	US-09-446-504-80	Sequence 80, Appl
18	374.5	7.0	335	3	US-09-712-266-80	Sequence 80, Appl
19	320.5	6.0	556	4	US-09-949-016-7424	Sequence 7424, Ap
20	310	5.8	444	4	US-09-248-796A-19305	Sequence 19305, A
21	306.5	5.7	465	4	US-09-949-016-10909	Sequence 10909, A
22	306.5	5.7	482	4	US-09-538-092-1308	Sequence 1308, Ap
23	306.5	5.7	482	4	US-08-624-735E-5	Sequence 5, Appl1
24	304	5.7	488	4	US-09-538-092-1367	Sequence 1367, Ap
25	303.5	5.7	433	4	US-08-624-735E-9	Sequence 9, Appl1
26	303.5	5.7	433	4	US-09-645-337A-13	Sequence 13, Appl
27	303	5.7	480	4	US-08-624-735E-10	Sequence 10, Appl
28	302	5.6	482	1	US-08-528-355A-1	Sequence 1, Appl1
29	302	5.6	482	1	US-08-717-365-1	Sequence 1, Appl1
30	296	5.5	448	4	US-09-248-796A-19163	Sequence 19163, A
31	288	5.4	513	4	US-09-645-337A-12	Sequence 12, Appl
32	278	5.2	517	3	US-09-282-305-8	Sequence 8, Appl1
33	278	5.2	517	3	US-09-883-720-8	Sequence 8, Appl1
34	277.5	5.2	488	3	US-09-282-305-2	Sequence 2, Appl1
35	277.5	5.2	488	4	US-09-883-720-2	Sequence 2, Appl1
36	277	5.2	111	4	US-09-270-767-49056	Sequence 33839, A
37	277	5.2	111	4	US-09-270-767-49056	Sequence 49056, A
38	276.5	5.2	349	4	US-09-252-991A-27544	Sequence 27544, A
39	275.5	5.1	2088	4	US-09-548-372D-13	Sequence 13, Appl
40	275.5	5.1	2088	4	US-09-548-367D-13	Sequence 13, Appl
41	275.5	5.1	2088	4	US-09-551-853D-13	Sequence 13, Appl
42	275.5	5.1	2088	4	US-09-548-376D-13	Sequence 13, Appl
43	275.5	5.1	2088	4	US-09-548-373D-13	Sequence 13, Appl
44	275.5	5.1	2088	4	US-09-548-366F-13	Sequence 13, Appl
45	275.5	5.1	2088	4	US-09-548-368D-13	Sequence 13, Appl

## ALIGNMENTS

RESULT 1  
US-09-849-602-18  
Sequence 18, Application US/09849602  
Patent No. 6794501  
GENERAL INFORMATION:  
APPLICANT: Scanlan, Matthew J.  
APPLICANT: Old, Lloyd J.  
APPLICANT: Stockert, Elisabeth  
APPLICANT: Chen, Yao-Tseng  
TITLE OR INVENTION: Colon Cancer Antigen Panel  
FILE REFERENCE: L0461/7105(JRV)  
CURRENT APPLICATION NUMBER: US/09/849,602  
CURRENT FILING DATE: 2001-05-04  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 18  
LENGTH: 897  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-849-602-18

Alignment Scores:  
Pred. No.: 4.97e-306  
Score: 4677.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 87.49%  
DB: 4  
Gaps: 0

US-09-502-945-2 (1-2885) X US-09-849-602-18 (1-897)

Qy 2 GAATTCCTCTTGGAGTGAAGTGAAGCCACACCCAGCGGCGCTCAACCATTCCTCCCA 61  
Db 1 GtupheuleuenserlySerlySgluProthPrdclYglYleuSnhlSserleuPro 20  
Qy 62 CACGACCCCAAAAGCTGGGAGCCACCATGCTTCTTGGACGAGATTCCCTCCCA 121

Db 21 GlnHisProLys-YserTrgIylAlaHisAlaSerLeuAspGlnSerProProGln 40  
QY 122 AGGGGGCCCCCTGAGAGGCGCTCCCTCTACAACTGCTTGGCTGGGCGCTTCAGACAGT 181  
Db 41 SerGlyProProGlyThrProProSerTrpLysLeuProLeuProGlyProLysAspSer 60  
QY 182 CGAGAGACTTCACCCCTCCGCAAAACAGCTCTGAACCCCACTTGAAGTCAAGTCCATCAAG 241  
Db 61 ArgAspAspPheIleuAlaGlySerThrAlaSerGluProAsnLeuLysValArgSerArg 80  
QY 242 CTAAACAGAGGTGGCTGACGGGAGAGCAAGTCCCTCTGGCTGGCAAGATGGGACT 301  
Db 81 LeuLysGlnLysValAlaGlyArgSerSerProLeuLysArgGlyAspGlyThr 100  
QY 302 GTTATTAGACCTTTAAAGAGAGGCTGTAGATCAAGATCCGGGCGCTGGGGGGCTG 361  
Db 101 ValIleSerThrPheLysValArgAlaValGlnIleThrGlyAlaGlyProGlyAlaSer 120  
QY 362 TCCGCTGTAAACAACGCAACCGGCTCCGAGCCCAAGCTTCCCAAGCTCCACAGAC 421  
Db 121 SerValCysAsnSerAlaProGlySerGlyProSerSerProAsnSerSerHisSerThr 140  
QY 422 ATGGCTGAGAAATGACTTTACTGGCTCAGTCCCAACATCCCACTGAGATGCTCCCTCAG 481  
Db 141 IleAlaGlnAsnGlyPheThrGlySerValProAsnIleProThrGluMetLeuProGln 160  
QY 482 CACCGAGCCCTCCCTCTGAGACAGTCCCAACAGTTCAGCTTCAAGTCTCCCTCT 541  
Db 161 HisArgAlaLeuProLeuAspSerSerProAsnGlnPheSerLeuLysTrpSerProSer 180  
QY 542 CTGCCCCAACAATCTTCTTACGGGCTGACGGCCACCGCTCACTGTCAACCACTCACTCACT 601  
Db 181 LeuProAsnIleSerIleuGlyLeuGlnAlaThrValThrValThrAsnSerHisIleuThr 200  
QY 602 GCGTCCCCGAGAGCTGTGACACACAGAGAGGCGGAGGCGCCCTCCAGTCCCTGGCG 661  
Db 201 AlaSerProLysLeuSerThrGlnGlnGlnAlaGlnArgGlnAlaLeuGlnSerLeuArg 220  
QY 662 CAGGGTGGACGCGTGAACCGGCAAGTTCATGAGACATCTTATTCCTGGCTCCCTGCTG 721  
Db 221 GlnGlyGlyThrLeuThrGlyLysPheMetSerThrSerSerIleProGlyCysLeuLeu 240  
QY 722 GCGGTGACATGGAAGGCGGAGCGGAGCGCCACCGAGCATCTCCCTGTGTGACAGATGTG 781  
Db 241 GlyValAlaLeuGlnGlyAspGlySerProHisGlyHisAlaSerLeuLeuGlnHisVal 260  
QY 782 CTGTGTGTGAGACAGCGCCGCGACAGAGCACTCTCATTTGCTGTGCACTCCACGGGCGAG 841  
Db 261 LeuLeuLeuGlnGlnAlaArgGlnGlnSerThrLeuIleAlaValProLeuHisGlyGln 280  
QY 842 TCCCACTAGTGAACGGGTGAACGTGTGGACCAACAGCATGGGACGGTGAAGCATCTCCG 901  
Db 281 SerProLeuValThrGlyLysArgValAlaThrSerIleArgThrValGlyLysLeuPro 300  
QY 902 CGGCACTCGGCGCTTACGCGCACTAGTCTCTCAACGCTGCGGAGAGTCCCGAGCGCTTG 961  
Db 301 ArgHisArgProLeuSerArgThrGlnInsSerProLeuProGlnInsProGlnAlaLeu 320  
QY 962 CAGCAGCTGGTCAATGCAACAACAGCACAGCAAGTCTTGGAGAAAGCAAGACAGCAGAG 1021  
Db 321 GlnGlnLeuValMetGlnGlnGlnHisGlnGlnPheLeuGlnLysGlnLysGlnGln 340  
QY 1022 CTACAGCTGGGCAAGATCTCAACCAAGACAGGGGAGCTGCGGAGCGCCACACCCAG 1081  
Db 341 LeuGlnLeuGlyLysIleLeuThrLysThrGlyGlyLeuProArgGlnProThrThrHis 360  
QY 1082 CCTGAGAGACAGAGAGAGAGCTGACGAGACAGACAGAGGCTTGTGCTGGGAGGAGAGCC 1141  
Db 361 ProGlnGlnThrGlnGlnGlnGlnLeuThrGlnGlnGlnValLeuLeuGlnGlyGlnGlyAla 380  
QY 1142 CTGACCATGCCCCCGAGAGGCGCTCCACAGAGTGAAGACACAGAGAAAGCTTGAAGAG 1201

Db 381 LeuThrMetProArgGlnGlySerThrGlnSerGlnSerThrGlnGlnLeuLeuGlnGln 400  
QY 1202 GAGACGAGAGAGAGATGGGAGAGAGAGAGATGTCATCCAGGTAAAGACAGAGAG 1261  
Db 401 GlnAspGlnGlnGlnAspGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 420  
QY 1262 GCGGAGAGTGTGCTGAGAGAGGCGCGCATTTGAGAGACCTGTGCTGGATTCAAAAA 1321  
Db 421 GlyGlnSerGlyAlaGlnGlnGlnGlnProAspLeuGlnGlnProGlyAlaGlyTrpLysLys 440  
QY 1322 CTGTCTTCAGAGCCCAACCGCTGCAACCTTTGACAGTGTACCAAGCGCGCTCAGCTCG 1381  
Db 441 LeuPheSerAspAlaGlnProLeuGlnProLeuGlnValTyrGlnAlaProLeuSerLeu 460  
QY 1382 GCCACTGTCCCCCAACAGCCCTGGGCGGTATCCCAATCTCCCTGCTGCGCGGCG 1441  
Db 461 AlaThrValProHisGlnAlaLeuGlyAlaGlnThrGlnInsSerSerProAlaAlaProGlyGly 480  
QY 1442 ATGAGAACCCCCCAGACCAACCCGTCAAGACCTTTCAACCAAGTGTGCTTAAGAC 1501  
Db 481 MetLysAsnProProArgGlnProValLysHisIleuPheThrThrSerValValTyrAsp 500  
QY 1502 ACCTTCATGCTTAAAGACCAAGTGCATGTGCGGGAACAACAACGTGACCTGAGCATGCT 1561  
Db 501 ThrPheMetLeuLysHisGlnCysMetCysGlyAsnThrHisValHisProGlnHisAla 520  
QY 1562 GCGCGGATCCAGAGCATCTGTGCTCCGCTGACAGAGACAGCGCTGTGATCAAGTGCAG 1621  
Db 521 GlyArgGlnGlnSerIleThrPheArgLeuGlnGlnThrGlyLeuLeuSerLysCysGln 540  
QY 1622 CGGATCCGAGGTGCAAAACCCAGTAAATGAGATCCAGACAGTGCATCTTGAATCCAC 1681  
Db 541 ArgIleArgGlyArgLysAlaThrLeuAspGlnIleGlnThrValHisSerGlyTrpHis 560  
QY 1682 ACCCTGCTTAAAGGACCAAGTCCCTCAACCGGCAAGCAACTGACAGCAAGAGTGTCTC 1741  
Db 561 ThrLeuLeuTrpGlyThrSerProLeuAsnArgGlnLysLeuAspSerLysLysLeuLeu 580  
QY 1742 GGTCCCATGACCCAGAAAGTATGCTGTGCTGCTTGTGGGGCAATCCGAGGTGACAGT 1801  
Db 581 GlyProIleSerGlnLysMetTrpAlaValAlaLeuProCysGlyGlyIleGlyAlaAspSer 600  
QY 1802 GACACCGTGTGAATGAGATGCATCTCTCAAGTCTGTGCGCATGGACAGTGGCTCCCTG 1861  
Db 601 AspThrValTrpAsnGlnMetHisSerSerSerAlaValArgMetAlaValGlyCysLeu 620  
QY 1862 CTGGAGCTGGCTTCAAGGTGGCTGACAGAGAGCTCAAAAGATTTGGCAATCATCCGG 1921  
Db 621 LeuGlnLeuAlaPheLysValAlaAlaGlyGlnLeuLysAsnGlyPheAlaIleIleArg 640  
QY 1922 CCCCAGACACCAACCGCAGAGATCCACAGCCATGGAGATTCGTCTTCAACTGTGA 1981  
Db 641 ProProGlyHisHisAlaGlnGlnGlnSerThrAlaMetGlyPheCysPhePheAsnSerVal 660  
QY 1982 GCCATCACCGCAAACTCTTACAGCAGAAAGTTGAACGTGGGCAAGGTCTCATGTGAC 2041  
Db 661 AlaIleThrAlaLysLeuLeuGlnGlnLysLeuAsnValGlyLysValLeuIleValAsp 680  
QY 2042 TGGGAATTCACCAATGGCAATGGCAACCGAGCGCTTCAAAATGACCCCTGTGGCTC 2101  
Db 681 TrpAspIleHisHisGlyLysAsnGlyThrGlnGlnAlaPheTrpAsnAspProSerValLeu 700  
QY 2102 TACATCTCTGTGATGCTATGACCAACGGGAACTTTCTTCAAGGCTCTGGGCGCTCGAA 2161  
Db 701 TyrIleSerLeuHisArgTrpAspAsnGlyAsnPhePheProGlySerGlyAlaProGln 720  
QY 2162 GAGGTGTGTGAGAGACAGAGCGTGGGTTCAATGTGAACGTGGCATGACAGAGGTGTG 2221  
Db 721 GluValGlyGlyGlyProGlyValGlyTrpAsnValAsnValAlaThrThrGlyGlyVal 740  
QY 2222 GACCCCCCATTTGAGAGAGTGAAGTACCTTACAGCTTCAAGCAAGTGTGATGCCCATT 2281  
Db 741 AspProProIleGlyAspValGlyTrpLeuThrAlaPheArgThrValValMetProIle 760



QY 2282 GCCCAGAGTTTCACCTGATGTGTCTAGTCTCCGCGGGTTTGTAGTGTGAAGGA 2341  
DB 761 AHHHbGluHeserProleuAValLeuValSerLaGlyPheAraLaValGluGly 780  
QY 2342 CATCTGTCTCTGTGGGTGCTACTGTGTACCCGACATGTTTGGCACTTGACCAGG 2401  
DB 781 HbLeuSerProleuGlyGlyTyrSerValThrAlaArgCySerPheGlyHbLeuThrArg 800  
QY 2402 CAGCTGATGACCTGGGACGGGGCGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2461  
DB 801 GlnLeuSerThrLeuAlaGlyGlyTyrValValLeuAlaLeuGluGlyGlyHbAraPhe 820  
QY 2462 ACCGGCATGT 2521  
DB 821 ThrAlaLeuCyAraPheAraSerGlyAlaCyValSerAlaLeuLeuSerValLysLeuGln 840  
QY 2522 CCCTTGATGAGGAGCTTTGACAGCAAAAGCCCAACATCAACGATGTGGCCACGCTAGAG 2581  
DB 841 ProleuAraGlyAlaValLeuGlnGlnLysProAraGlnLeuAlaValAlaThrLeuGln 860  
QY 2582 AAAGTCATGAGATCCAGACAAACACTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2641  
DB 861 LysValIleGlyIleGlnSerLysHbAraPheSerCyValGlnLysPheAlaAlaGlyLeu 880  
QY 2642 GGGCGGTCCTGGGAGGGGGCCCAAGAGCTGAGACCGGAAGCCGAAATG 2692  
DB 881 GlyAraSerLeuAraGlyAlaGlnAlaGlyGlnThrGluAlaGlnLeu 897

RESULT 2  
US-09-637-145-4  
Sequence 4: Application US/09637145  
Patent No. 6673587  
GENERAL INFORMATION:  
APPLICANT: EVANS, RONALD M.  
APPLICANT: KAO, HUNG-YING  
APPLICANT: DOMES, MICHAEL  
APPLICANT: ORDENLICH, PETER  
TITLE OF INVENTION: NOVEL HISTONE DEACETYLASE, AND USES THEREFOR  
FILE REFERENCE: SALK3000  
CURRENT APPLICATION NUMBER: US/09/637,145  
CURRENT FILING DATE: 2000-08-11  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 1114  
TYPE: PRT  
ORGANISM: Mus sp.  
US-09-637-145-4

Alignment Scores:  
Pred. No.: 3,54e-298 Length: 1114  
Score: 4560.50 Matches: 888  
Percent Similarity: 96.70% Conservative: 19  
Best Local Similarity: 94.67% Mismatches: 25  
Query Match: 85.31% Indels: 7  
Gaps: 2

US-09-502-945-2 (1-2885) x US-09-637-145-4 (1-1114)

QY 2 GAATTCCTTGTGAGTCAAGAGAGCCACACGAGGAGCTTCAACATTCCTCCCA 61  
DB 181 GlnPheLeuLeuSerLysSerLysGlnProThrProGlyGlyLeuAraHbAraSerLeuPro 200  
QY 62 CAGCAGCCCAATGCTGGGAGCCACACATGCTTTTGAACAGATTCCTCCCGAG 121  
DB 201 GlnHbAraProLysCySerTrpGlyAlaHbAraLeuAraSerLeuAraGlnSerProGln 220  
QY 122 AGGAGGCGCCCTGGAGAGCTCCCTCTCAAAATGCTTGGCTGGGCGCTTACGAAAGT 181  
DB 221 SerGlyProProGlyThrProProSerLysLysLeuProLeuGlnProGlyTyrAraSer 240  
QY 182 CGAGAGAGCTTCCCGCCGAAAGAGCGCTGTGACCCCAACTTGAAAGTGCCTTCAAG 241

DB 241 ArgAraPhePheProLeuAraGlySerThrAlaSerGlnProAraLeuLysValAraSerArg 260  
QY 242 CTAAACAGAAAGGTGTGAGCCGAGAGAGAGATGCCCTCTGTGGTGGCAAGATGGGACT 301  
DB 261 LeuLysGlnLysValAlaGlnAraGlySerSerProLeuLeuAraGlyLysAraGlyThr 280  
QY 302 GTTATTAGCAGCTTTAAGAAAGAGCTGTGATGATCAAGATCCGAGGCTGGGAGCTGC 361  
DB 281 ValIleSerThrPheLysLysAraGlyAlaGlnIleThrGlyThrGlyProGlyValSer 300  
QY 362 TCCGTGTGAACAGGAGCCGAGCTCCGAGCTCCAGCTTCCCAAGCTCCACAGACC 421  
DB 301 SerValCyAraSerAlaProGlySerGlyProSerSerProAraSerAlaSerThr 320  
QY 422 ATGCTGAGAAATGGCTTTATGTGCTAGTCCCAACATCCCACTGAGATGCTCCCTCAG 481  
DB 321 IleAlaGlnAraGlnIlePheThrGlySerValProAraGlnProThrGlnMetIleProGln 340  
QY 482 CAGCAGCCCTCCCTGTGACAGCTCCCAACAGCTTCAAGCTTCAAGCTTCTCTT 541  
DB 341 HbAraGlnLeuProLeuAraPheSerSerProAraGlnPheSerLeuThrThrSerProSer 360  
QY 542 CTGCCCAACATCTCCCTGAGGCTGCAAGCCAGCTCACTGTCAACATCAGACTCACT 601  
DB 361 LeuProAraHbAraLeuGlnLysLeuGlnAlaThrValThrValThrAraSerHbAraLeuThr 380  
QY 602 GCTCCCGCAAGCTGTGACACAGCAGAGAGCCGAGAGAGGCGCTCCAGTCCCTGGCG 661  
DB 381 AlaSerProLysLeuSerThrGlnGlnGlnAlaGlnAraGlnAlaLeuGlnSerLeuAraG 400  
QY 662 CAGGATGAGAGCTGACCGGCAAGTTCAATGACATCTCTTATCTGTGCTGCTGCTGCTG 721  
DB 401 GlnGlyGlyThrLeuThrGlyLysPheMetSerThrSerSerIleProGlyCybLeuLeu 420  
QY 722 GAGGTGACATGAGAGGAGCGAGAGGAGCCGAGGAGATGCTCCCTGTGACAGATGTG 781  
DB 421 GlyValAlaLeuGlnLysAraPheThrSerProHbGlyHbAraSerLeuGlnHbAraVal 440  
QY 782 CTGTGTGTGAGAGAGCGGCGAGAGAGACCTCACTTGTGTGTGTGTGTGTGTGTGTGTGTGT 841  
DB 441 -CySerTrpThr--GlyAraGlnGlnSerThrLeuIleAlaValProLeuHbAraGlyGln 460  
QY 842 TCCCACTGATGACGGGTGAACGTGTGACCAAGCATGAGAGAGGAGCAAGTCCGCG 901  
DB 460 SerProLeuValThrGlyLysAraGlyAlaThrSerMetAraGlyThrValGlybLeuPro 420  
QY 902 CGGATCGGCGCTGAGCCGACCTCACTCACTCACTGCGGAGATGCCAGGCGCTG 961  
DB 480 ArgHbAraPheProLeuSerAraGlnGlnSerSerProLeuProGlnSerProGlnAlaLeu 499  
QY 962 CAGCAGCTGATGACAGCAACAGCAGCAGAGTTCCTGAGAAAGCAAGAGCAGCAG 1021  
DB 500 GlnGlnLeuValMetGlnGlnGlnHbAraGlnPheLeuGlnLysGlnLysGlnGln 519  
QY 1022 CTACAGCTGGGCAAGATCTCCCAAGAGAGAGGAGTGGCCAGGAGCCACCAACCCAC 1081  
DB 520 MetGlnLeuGlyLysLysLeuThrLysThrGlyLeuLeuSerAraGlnProThrHbAra 539  
QY 1082 CTTGAGAGACAGAGAGAGCTGACGAGACAGAGAGTCTTGTGGGAGAGAGGCC 1141  
DB 540 ProGlnLysThrGlnLysGlnLysLeuThrGlnGlnGlnAlaLeuLeuGlnGlyGlyAla 559  
QY 1142 CTGACATGCGCCGAGAGGCTCCACAGAGTGAAGACACAGAGAACTGAGAGAG 1201  
DB 560 LeuThrIleProAraGlnLysSerThrGlnSerGlnSerThrGlnLysPheLeuGlnGln 579  
QY 1202 GAGAGAGAGAAAGATGAGGAGAGAGAGAGATTCATCCAGGTTAAGAGCAGAGAG 1261  
DB 580 GlnGlnGlnLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 598  
QY 1262 GAGGAGAGTGTGCTGAGAGGAGGCGGAGCTTGTGAGAGAGCTGTGATCAAAA 1321

```

Db      599 GLyGluSerGlyProAspGluGlyProAspLeuGluSerSerAlaGlyTyrTyrValys 618
QY      1322 CTGTCTTCAGATGCCCAACCGCTGCAACCTTTCAGAGGTATACCAAGCGCCCTCAGGCTG 1381
Db      619 LeuPheAlaMetAlaGlnGlnLeuGlnProLeuGlnValTyrGlnAlaProLeuSerLeu 638
QY      1382 GCCACTGTGTG-CCCAACCAAGCCCTGGGCGGTACCCCAATCTTCCTGCTGCTGCGGCGGC 1441
Db      639 AlaThrValProHisGlnAlaLeuGlyArgThrGlnSerSerProAlaAlaProGlySer 658
QY      1442 ATGAAGACCGCCCAAGCAACCC-----GTCAAGACCTCTTTCACCAAGGTGTC 1495
Db      659 MetLeuSerProThrAspGlnProThrValValTyrHisLeuPheThrThrGlyValVal 678
QY      1496 TACGACACGTTTACGTAAAGACACAGTGCATGTGCGGAAACAACAAGTGCACCTGAG 1555
Db      679 TyrAspThrLeuMetLeuTyrHisGlnCysMetCysGlyAsnThrHisValHisProGlu 698
QY      1556 CATGCTGGCCGATCCAGAGCATGTGGTCCCGCTGCAGAGACAGAGGCTGCTTACGACAG 1615
Db      699 HisAlaGlyArgGlnSerIleTyrSerArgLeuGlnGlnThrGlyLeuLeuGlyLys 718
QY      1616 TGGAGCGGATCCGAGGTTGCAAAAGCCAGCTGATGATGATCCAGACAGTGCACCTGGA 1675
Db      719 CysGlnTyrGlnLeuArgTyrGlyAlaThrLeuAspGlnIleGlnThrValHisSerGlu 738
QY      1676 TACCAACACCTTCTATATGGAGCAGTCCCTCAACCGGCAAGAGTACAGACAGAAAG 1735
Db      739 TyrHisThrLeuLeuTyrGlyThrIleSerProLeuHisAlaGlnIleValLeuAspSerTyrLys 758
QY      1736 TTGCTCGGTCCCATCAGCCCAAGAGATGATGCTGTGCTGCTGCTGCGGCGCATCGGGGTG 1795
Db      759 LeuLeuGlyPrcIleSerGlnLysMetTyrAlaMetLeuProCysGlyGlyIleGlyVal 778
QY      1796 GACAGTGACACCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1855
Db      779 AspSerAspThrValTyrAsnGlnMetHisSerSerSerAlaValAlaMetAlaValGly 798
QY      1856 TGCCTGTGAGATGAGCTTCAAGGTGCTGCAAGAGAGCTCAAGATGATGATGATGATGATG 1915
Db      799 CysLeuValGlnLeuAlaPheLysValAlaAlaGlyValLeuLysAsnGlyPheAlaIle 818
QY      1916 ATCCGCGCCCAAGACAGACACCGCGGAGGATCCACAGCCATGGGATTCCTCTTTCAC 1975
Db      819 IleArgProProGlyHisHisAlaGlnGlnSerThrAlaMetGlyPheCysPhePheAsn 838
QY      1976 TCTGTAGCCATCAACGCAAACTCTACAGACAGAGTGAACGATGATGATGATGATGATGATG 2035
Db      839 SerValAlaIleThrAlaLysLeuLeuGlnGlnLysLeuSerValGlyLysValLeuIle 858
QY      2036 GTGAGCTGGAGACATTCACATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 2095
Db      859 ValAspTyrAspIleHisHisGlyAsnGlyThrGlnIleAlaPheTyrAlaAspProSer 878
QY      2096 GTGCTTACATCTCTCTGCAATCGCTATGACAAGGGAATCTTTCAGGCTCTGGGCT 2155
Db      879 ValLeuTyrIleSerLeuHisArgTyrAspAsnGlyAsnPhePheProGlySerGlyAla 898
QY      2156 CCGAAGAGGTTGATGAGACACAGCGGTGGGGTGAACATGGAACGCGGATGAGACAGCA 2215
Db      899 ProGlnIleValGlyGlyValProGlyValGlyTyrAsnValAsnValAlaIleProGly 918
QY      2216 GGTGTGAGACCCCATTTGAGACGTTGATGATGATGATGATGATGATGATGATGATGATG 2275
Db      919 GlyValAspProProIleGlyAspValGlyTyrLeuThrAlaPheArgThrValValMet 938
QY      2276 CCGATTGCCACAGATTTCTACCTGATGTGCTCTTCTGCGCGGGGTTGATGCTGTT 2335
Db      939 ProIleAlaGlnGlnLysHisSerProAspValValLeuValSerAlaGlyPheAspAlaVal 958
QY      2336 GAAGGACATGCTGCTCTCTGGGGGTGCTACTGCTGACCGCGAGATGTTTGGCAATGG 2395
Db      959 GlnGlyHisLeuSerProLeuGlyGlyTyrSerValThrAlaArgCysPheGlyHisLeu 978

```

```

QY      2396 ACCAGGACCTGATGATCCCTGGAGGGGGCCGGGTGTCTGCTGCTGAGAGGAGCCAT 2455
Db      979 ThrArgGlnLeuMetThrLeuAlaGlyArgValValLeuAlaLeuGlnGlyGlyHis 998
QY      2456 GACTTGACCGGCATCTGTATGATCCCTCTGAGGCTGTGTGTGCTGCTGCTGCTGCTGCTG 2515
Db      999 AspLeuThrAlaIleCysAspAlaSerGlnAlaCysValSerAlaLeuLeuSerValGlu 1018
QY      2516 CTGACGACCTTGATGAGACAGTCTTGCAGCAAAAGCCCAACATCAACGACGTGGCAGC 2575
Db      1019 LeuGlnProLeuAspGlnAlaValLeuGlnGlnLysProSerValAsnAlaValAlaThr 1038
QY      2576 CTAGAGAAATCATATCAGATTCAGACAGCAAACTGAGGCTGTGTGCAAGATTGCGCGCT 2635
Db      1039 LeuGlnLysValIleGlnIleGlnSerLysHisTyrSerCysValGlnArgPheAlaIle 1058
QY      2636 GGTCTGGCGCGGTCTGCTGAGAGGGGCCCAAGCAGGTGAACCGAAGAACCCGAAT-GrG 2694
Db      1059 GlyLeuGlyCysSerLeuArgGlnAlaGlnThrGlyGlyLeuGlnAlaGlnThrVal 1078
QY      2695 AACGCCATGGCTTGTGTTGGTGGGGGCCGAACAGGCGCAAGCTGCGCAGCGCGGAA 2754
Db      1079 SerAlaMetAlaLeuLeuSerValGlyAlaGlnGlnAlaGlnAlaValAlaThrGlnGlu 1098
QY      2755 CACAGCCCAAGCGCGGACAGAGAGCCCATGAGACAGAGACCTGCGCTG 2802
Db      1099 HisSerProArgProAlaGlnGlnProMetGlnGlnGlnProAlaLeu 1114

RESULT 3
US-09-644-827B-9
; Sequence 9, Application US/09644827B
; Patent No. 6762283
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: SCHUCHMANN, Marcus
; APPLICANT: GONCHAROV, Tanya
; TITLE OF INVENTION: Caipase-8 Interacting Proteins
; FILE REFERENCE: WALLACH=26
; CURRENT APPLICATION NUMBER: US/09/644,827B
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 132105
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 127721
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1041
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-644-827B-9

Alignment Scores:
Pred. No.: 1,276-172 Length: 1041
Score: 2691.00 Matches: 568
Percent Similarity: 71.38% Conservative: 118
Best Local Similarity: 59.11% Mismatches: 195
Query Match: 50.34% Indels: 81
DB: 4 Gaps: 23

US-09-502-945-2 (1-2885) x US-09-644-827B-9 (1-1041)
QY      2 GAATTCCTCTGTCGATGCAAGGAGCCACAGCGGCGCTCAACATTCCTCCCA 61
Db      134 GluPheValLeuAsnLysLysValAlaLeuAlaHisArgAsnLeuAsnHisCysIleSer 153
QY      62 CAGCACCCTCAATGCTG-----GGAGCCCAACATGCTTTTGGACCAAGATTCCCT 115
Db      154 SerAspProArgTyrThrTyrGlyLysThrGlnHisSerSerLeuAspGlnSerSerPro 173
QY      116 CCCCAGAGGGGCGCCCTGGAGGCTCCCTCTAATAAATGCTTGTGCTGGGCGCTAC 175

```



QY 2261 AGGACAGTGTGATGCCATTGCCCCAGAGTCTCACCTGATGCTGCTAGTCTCGGCC 2320  
|||  
Db ArgThrValValMetProIleLeuSerGlnPheAlaProAspValValLeuValSerSer 888  
QY 2321 GGGTTTGAACGCTGTGAAGACATCTGTCTCTCTGCTGCTGCTACTCTGTACCCGCCAGA 2380  
|||  
Db GlyPheAspAlaValGlnGlnPheProThrProLeuGlyGlyTrpAsnLeuSerAlaArg 908  
QY 2381 TGTGTTGGCAGCTTGAACAGGAGCTGATGACCTGGCAGAGGAGCCGGGTGCTGCTGCC 2440  
|||  
Db CyPheGlyTrpLeuThrTrpGlnLeuMetGlyLeuAlaGlyAlaGlyIleValLeuAla 928  
QY 2441 CTGAGGAGGAGCCCATGACCTTGACCGCATGTGATGCTCTGAAGCTTGCTGCTGCT 2500  
|||  
Db LeuGlnGlyTrpIleAspLeuThrAlaIleCysAspAlaSerGlnAlaCysValSerAla 948  
QY 2501 CTGCTCAGTTAAAGCTGAGCCCTTGATGAGGAGCTTTGACGAAAGCCCAACATC 2560  
|||  
Db LeuLeuGlyTrpAsnGlnLeuAspProLeuProGlnLeuValLeuGlnGlnArgProAsnAla 968  
QY 2561 AACGAGTGGCCAGCTAGAGAAAGTCAATGAGATCCAGAGCAAAACTGAGAGCTGTG 2620  
|||  
Db AsnAlaValArgSerMetGlnValMetGlnIleHisSerTrpTrpArgCysLeu 988  
QY 2621 CAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2680  
|||  
Db GlnArgThrTrpSerThrAlaGlyArgSerLeuIleGlnAlaGlnThrCysGlnAsnGln 1008  
QY 2681 GAAGCCGGAATGTGAAGCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2739  
|||  
Db 1009 GlnAlaGlnThrValThrAlaMetAlaSerLeuSerValGlyValAlaProAlaGln 1027  
QY 2740 GCGGAGCCGCGAGAACAGAGCCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2799  
|||  
Db 1028 -----LysArgProAspGlnGlnProMetGlnGlnGlnProPro 1040  
QY 2800 CTG 2802  
|||  
Db 1041 Leu 1041

RESULT 4  
US-09-637-145-3  
; Sequence 3, Application US/09637145  
; Patent No. 6673587  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, RONALD M.  
; APPLICANT: KAO, HUNG-YING  
; APPLICANT: DOMENIS, MICHAEL  
; APPLICANT: ORDENTLICH, PETER  
; TITLE OF INVENTION: NOVEL HISTONE DEACETYLASE, AND USES THEREFOR  
; FILE REFERENCE: SALK3000  
; CURRENT APPLICATION NUMBER: US/09/637,145  
; CURRENT FILING DATE: 2010-08-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 1084  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-637-145-3

Alignment Scores:  
Pred. No.: 1,284-172 Length: 1084  
Score: 2691.00 Matches: 568  
Percent Similarity: 71.36% Conserved: 118  
Best Local Similarity: 59.11% Mismatches: 195  
Query Match: 50.34% Indels: 81  
Gaps: 23

US-09-502-945-2 (1-2885) x US-09-637-145-3 (1-1084)  
QY 2 GAATTCCTTTGTAAGTCAAGAGCCCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 61  
|||||:|||||:|||||  
|||||:|||||:|||||

Db 177 GlnPheValLeuAsnLysLysValAlaLeuAlaHisArgAsnLeuAsnHisCysValSer 196  
QY 62 CAGACACCCCAATGCTG-----GGAGCCCAACATGCTTTTGGACGAGATTCCTCC 115  
|||  
Db 197 SerAspProArgTrpTrpGlyGlySerGlnHisSerSerLeuAsnSerPro 216  
QY 116 CCCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 175  
|||  
Db 217 ProGlnSer-----GlyValSerThrSerTrpAsnHisProValLeuGlyMetTrp 233  
QY 176 GACAGTCGAGAGGAGCTTCCCTCCGCAAAAGAGCTTGAAGCCCACTGAAGAGGCT 235  
|||  
Db 234 AspAlaLeuAspAspPheProLeuArgLysTrpAlaSerGlnProAsnLeuLysLeuArg 253  
QY 236 TCAGAGCTTAAACAGAAAGTGGCTGAGCCGAGAGAGAGTCCCTCTGCTGCTGAGAT 295  
|||  
Db 254 SerArgLeuLysGlnLysValAlaGlnLysArgSerProLeuLeuArgTrpLysArg 273  
QY 296 GGGAGCTGTATTAGACCTTTAAGAAAGAGAGCTTTGAGATCAACAGTCCCGGAGCTGG 355  
|||  
Db 274 GlyProValValThrAlaLeuLysLysArgProLeuAspValThr----- 288  
QY 356 GCGCTCTCCGTGTGTAACAGCGGAGCCGCTCCGCGCCAGCTCTCC---AAGAGCTCC 412  
|||  
Db 289 ---AspSerAlaCysSerSerAlaProGlySerGlyProSerSerProAsnAsnSer 307  
QY 413 CACAGACACATGCTGAGATGAGCTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 472  
|||  
Db 308 GlySerValSerAlaGlnAsnGlyIleAlaProAlaValProSerIleProAlaGlnThr 327  
QY 473 CTCCCTCAGACCCGAGCCCTCCCTCTGAGACAGTCCCAACAGTTCAGCTTACAG 532  
|||  
Db 328 SerLeuAlaHisArgLeuValAlaArgGlnGlySerAlaAlaProLeuProLeuTrp 347  
QY 533 TCTCCTTCTCTGCGCAACATCTCCCTGAGGCTGAGCCAGCGTCACTGACCAACTCA 592  
|||  
Db 348 SerProSerLeuProAsnIleThrLeuGlyLeuProAlaThr----- 361  
QY 593 CACCTCAGTGCCTCCCGAAGCTGTGACA-----CAGCAGAGGAGCCGAGGAGGAGG 646  
|||  
Db 362 -----GlyProSerAlaGlyThrAlaGlyGlnAlaAspThrGlnThr 377  
QY 647 CTCAGTCCCTGCGGAG-----GTTGCAAGCTGACCGGAAATTCAATG 691  
|||  
Db 378 LeuProAlaLeuGlnGlnArgLeuSerLeuPheProGlyThrHisLeuThrProTrpLeu 397  
QY 692 AGCAGATCCTCTATTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 751  
|||  
Db 398 SerThrSer-----ProLeuGlnArgAspGlyAla 408  
QY 752 CAGGAGATGCTCCCTGCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 811  
|||  
Db 409 ---AlaHisSerProLeuLeuGlnHisMetValLeuLeuGlnGlnProProAlaGlnAla 427  
QY 812 ACCCTCATT-----GCTGTGCACTTCCAGCGGAGTCCCACTGATGACGGT 859  
|||  
Db 428 ProLeuValThrGlyLeuGlyAlaLeuProLeuHisAlaGlnSer---LeuValGlyAla 446  
QY 860 GAACGTGTGGCCACAGCATGCGGAGGTAGAGGATCCCGGAGATGGGCGCCGAGAGC 919  
|||  
Db 447 AspArgValSerProSer-----IleHisLeuLeuArgGlnHisArgProLeuGly 463  
QY 920 CGCAGTCAGTCTCAGCGCTGCGGAGAGTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 979  
|||  
Db 464 ArgThrGlnSerAlaProLeuProGlnAsnAlaGlnAlaLeuGlnHisLeuValIleGln 483  
QY 980 CAAAGCAGCAGGAGTCTTCTGAGAAAGCAGAG-----CAGCAGCAGTACAG 1027  
|||  
Db 484 GlnGlnHisGlnGlnPheLeuGlnLysHisLysGlnGlnPheGlnGlnGlnGlnGln 503  
QY 1028 CTGAGGCAAGATCTTCAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1087  
|||  
Db 504 MetAsnLysIleIleProLysProSerGlnProAlaArgGlnProGlnSerHisProGln 523



US-09-538-092-1222

## Alignment Scores:

Prod. No.:	1,28e-172	Length:	1084
Score:	2591.00	Matches:	568
Percent Similarity:	71.38%	Conservative:	118
Best Local Similarity:	53.11%	Mismatches:	195
Query Match:	50.34%	Indels:	81
DB:	4	Gaps:	23

US-09-502-945-2 (1-2885) X US-09-538-092-1222 (1-1084)

```

QY      2 GAATCTCTTTCGAAGTCAAGAGCCCAACAGCGGCGCTCAACATCTCTCCCA 61
Db      177 GluPheValLeuAsnIlySlySaIaLeuAlaHieArgAsnIleuHnHiscyIleSer 136
QY      62 CAGACCCCAAAAGCTGG-----GAGGCCACCAAGCTTCTTGGACAGAGTCCCT 115
Db      197 SerAspProArgTyrTyrGlyIySlyThrGlnHisSerSerIleuAspGlnSerPro 216
QY      116 CCCGAGAGCGGCCTCCCTGGAGCGCTCCCTCTCAAAATGCGCTTGGCGGCGCTAC 175
Db      217 ProGlnSer-----GlyValSerThrSerTyrAsnHieProValIleuGlyMetTyr 233
QY      176 GAGAGTGGAGACACTTCCCTCCGCAAAACAGCTTGAACCAATTGAAGTGGCT 235
Db      234 AspAlaIyAspAspPheProIeuArgIyThrAlaSerGluProAsnIleuIySlyLeuArg 253
QY      236 TCAAGCTTAACAGAAAGTGGCTGAGCGGAGAGAGCAAGCTCCCTCTGCGTCCAGAGAT 235
Db      254 SerArgLeuIySgIlnIySlyValaIaGlnIyArgSerSerProIeuAspArgIyAsp 273
QY      296 GGAGCTGTATTAACACCTTAAGAGAGAGAGCTGATGATCAAGGTGCGGCGCTGGG 355
Db      274 GlyProValIyThrAlaIeuIySlySargProIeuAspValThr----- 288
QY      356 GCGCTGCTCGGTATTAACAGCGCACCGGCTCGGCGCCAGCTCTGCC--AAAGCTCC 412
Db      289 ---AspSerIaCySerSerSerAlaProGlySerGlyProSerSerProIeuAsnSerSer 307
QY      413 CACAGACCAATCGTGAAGATGGCTTTACTGCTCAAGTCCCAACATCCCACTGAGATG 472
Db      308 GlySerValSerIaGlnIySgIlnIyLeaIaProAlaValProSerIleProAlaGlnThr 327
QY      473 CTCCTTCAGACGAGCGCTCCCTCTGACAGACTCCCAACAGATTCAAGCTCTACAG 532
Db      328 SerLeuAlaHieArgLeuValaIaArgGlyGlySerAlaIaIaProIeuProIeuTyrThr 347
QY      533 TCTCTTTCTGTGCCAAGATCTCCCTAAGGCTGCAAGGCCAAGCTCACTGCACCAACTCA 592
Db      348 SerProSerIeuProAsnIleThrIleuGlyIleuProAlaThr----- 361
QY      593 CACCTCACTGCCCTCCGAAAGCTGTGACA-----CAGCAGAGAGCCGAGAGAGGCC 646
Db      362 -----GlyProSerAlaGlyThrAlaGlyIyGlnIyAspThrIyGlnIyGlyLeuThr 377
QY      647 CTCAGAGCTCTGCGACAG-----GGTGCAGCGCTGACCGGCAAGTTCAAG 691
Db      378 LeuProAlaIeuGlnIyGlnIyGlySerIeuPheProGlyThrHieIleuThrProTyrIleu 397
QY      692 AGCAGCATCTCTATTCTGTGCTGCTGCGGCTGAGCACTGAGAGGCGAGCGGAGCCCC 751
Db      398 SerThrSer-----ProIeuGlnIyArgAspGlyIyAla 408
QY      752 CAGGGGCAATGCCCTCTGCTGACAGATGCTGTGTTGTCGACAGAGCGCGGACAGAGC 811
Db      409 ---AlaHisSerProIeuIeuGlnIyHieMetValIeuIeuGlnIyProProAlaGlnAla 427
QY      812 ACCCTCAT-----GCTGTCACATCCACAGGAGAGTCCCACTAGTGAAGCGGT 859
Db      428 ProIeuValIyThrGlyIeuGlyAlaIeuProIeuHieIaIaGlnSer---LeuValIyGlyAla 446
QY      860 GAACTGTGGCAACGAGCATGCGGACGGTAGGCAAGCTCCCGCGGCAATCGGCGCTGAGC 919

```

```

Db      447 AspArgValSerProSer-----IleHieIySlyLeuArgGlnHieIaArgProIeuGly 463
QY      920 CGCAGCTCAGTCCCTCAACGCTGCGGAGAGATCCCAAGCGCTGAGAGCTGATGACA 979
Db      464 ArgThrGlnSerAlaProIeuProGlnIyAsnIaIaGlnAlaIeuGlnHieIleuValIleGln 483
QY      980 CAACAGCACACAGAGATCTCTGAGAAAGAGAAAG-----CAGCAGCAGCTTACAG 1027
Db      484 GlnGlnHieGlnIlePheIeuGlnIySlySgIlnGlnIlePheGlnIleGlnIleuGln 503
QY      1028 CTGGGCAAGATCTCAACAGAGAGAGAGCTGCCAGGAGCCCAACCCACCTGAG 1087
Db      504 MetAsnIySleIleProIySerProSerGlnProAlaIyArgGlnProGlnIleHieIaProGln 523
QY      1088 GAGCAGAGAGAGAGCTGACGAGAGAGAGAGTCTTGTGGGAGGAGGAGCGCTG--- 1144
Db      524 GlnThrGlnIleGlnIleuIeuArgIlnHieSgIln---AlaIeuIeuAspGluProTyrIleuAsp 542
QY      1145 ACCATGCCCCGGAGGAGCTCCACAGAGAGTGAAGACACAGAGAGCTGAGAGAGAG 1204
Db      543 ArgLeuProGlyIyGlnIySgIlnIaHieIaIaGlnAlaGlyValGln---ValIySgIlnIy 561
QY      1205 GAGCAGAAAGAGATGGGAGAGAGAGAGATTCATCCAGTTAAGACAGAGAGGC 1264
Db      562 ProIleGlnSerAspGlnIleGlnIyAlaGln-----ProProArgIyVal 576
QY      1265 GAGAGTGTGTGAGAGAGGAGGCGGACCTTGAAGAGAGCTGAGTGAATACAAAAGT 1324
Db      577 GluProGlyGlnIyArgIln---ProSerGlnIleGlnIleuIeuPheArgGlnIleAlaIeu 595
QY      1325 TTCTCAGATGCCCAACCGGTGCAACCTTTCAGAGTGAACCAAGCGCCCTCAAGCTGACC 1384
Db      596 IeuIeuGlnIleGlnIyArgIlnIeHieSgIlnIyArgAsnTyrGlnIaIaSerMetGlnIaIa 615
QY      1385 ACTGTGCC-----CACCAAGCTTGGGCGGTACCAATCTCCCTGCT 1429
Db      616 GlyIleProValSerPheGlyGlyHieIaArgProIeuSerArgIaIaIleSerProAla 635
QY      1430 GCC-----CCTGGGAGCAAGAAACCCCAAGCAGCAACCCGTCAGACACTCTTC 1480
Db      636 SerAlaThrPheProAlaSerValGlnGlnIyProProThrIyAspPro-----ArgPhe 652
QY      1481 ACCCAAGTGTGTCTTACAGACATTCATGCTTAAGACACAGTGCATGTGGGGAACACA 1540
Db      653 ThrThrGlyIeuValIyThrAspThrIleuMetIeuIyHieGlnIySerIySgIySerSer 672
QY      1541 CAGCTCAGCTGAGAGATGCTGGCGGATCCAGAGACATCTGTGTCGCGCTGACAGAGACA 1600
Db      673 SerSerHieProGlnIyHieIaIyArgIleGlnSerIleTyrSerArgIeuGlnIyThr 692
QY      1601 GGCCTGTTAAGCAAGTGGCGAGGATCCGAGGTCGCAAGGCCAGCTGATGATGATCCAG 1660
Db      693 GlyIleuArgIlyIySeySgIlnIyIeArgGlyIyArgIyAlaIaThrIeuGlnIleuGln 712
QY      1661 ACAGTCACTCTGAATATACACACCTCTCTATTGAGCAGAGTCCCTCAACCGGCAAG 1720
Db      713 ThrValHieSerGlnIaHieIaThrIleuIeuTyrGlyThrAspProIeuAsnArgIlnIy 732
QY      1721 CTAGACAGCAAGAGTTGCTCGGTCCCATCAGCAGAAAGATGATGCTGTGCTGCTTGT 1780
Db      733 LeuAspSerIySlySeyIeuIeuGlnIySerIeuAla---SerValPheValArgIeuProCys 751
QY      1781 GGGGAGCATGGGGTGGACAGTGCACAGTGGAGATGATGATGATGATGATGATGATG 1840
Db      752 GlyGlyValGlyIyAlaIaSerIeAspThrIleTyrPheGlnIyAlaHieSerAlaGlyAlaIa 771
QY      1841 CGCATGAGAGTGGCTGCTGCTGCTGAGTGGCTTCAAGAGTGGCTGACAGAGACTCAAG 1900
Db      772 ArgIleuAlaValGlyIySeyValIyGlnIleuValPheIyValaIaIaThrGlyIleuIyS 791
QY      1901 AATGATTTGGCATCTCCGCGCCCAAGACACAGCGGAGGAATCCACAGCCATGGA 1960

```



```

Dh      792  AaaglyPheAlaValValArgProProGlyHnShhSAlaGluGluSerThrProMetCly 811
Qy      1961  TTGTGCTCTTCAACTGTGTAGCCATCAACCCGAAATCTCTACAGCAAGATTGAAGTGTG 2020
Dh      812  PheCysTyrPheAsnSerValAlaValAlaIaIaLysLeuLeuGlnGlnArgLeuSerVal 831
Qy      2021  GGCAAGGCTCATGTGTGAGCACTGGGAGCAATTGACCACTGGCAATTGGCAACCCAGCGCTTC 2080
Dh      832  SerLysIleLeuIleValaAspTrpAspValHnShhGlyAsnGlyThrGlnGlnAlaPhe 851
Qy      2081  TACAATGACCCCTGTGTCTCTACATCTCTGTGCATCGCTGATGACAGGGAACTTCTTT 2140
Dh      852  TyrSerAspProSerValLeuTyrMetSerLeuHnShhGlyTrpAspAspGlyAsnPhePhe 871
Qy      2141  CCAGGCTCTGGAGGCTCTGAAAGAGTTGATGAGAGCAAGGCGTGGAGTACAAATGTGAAC 2200
Dh      872  ProGlySerGlyAlaProAspGlyValGlyHnThrGlyProGlyValGlyPheAsnValAsn 891
Qy      2201  GTGGCATGGAACAGAGGTGTGGAGCCCGCCCATTTGGAGACGCTGAGATCACTTACAGCTTC 2260
Dh      892  MetAlaPheThrGlyGlyLeuAspProPheMetGlyAspAlaGlyTyrLeuAlaAlaPhe 911
Qy      2261  AGGACAGGTGATGATGCGCATTTGGCCGACAGAGTTCTACCATGATGTGGTCTTATGCTCCGC 2320
Dh      912  ArgThrValAlaMetProIleAlaSerGluPheAlaProAspValValLeuValSerSer 931
Qy      2321  GGGTTTGAATGCTGTGGAAGACATCTGTCTCTCTCTGGGTGGCTACTCTGTACACCGCAGA 2380
Dh      932  GlyPheAspAlaValGluGlyHnIleProThrProLeuGlyGlyTyrAsnLeuSerAlaArg 951
Qy      2381  TGTTTTGGCCACTTGACCAAGGCAAGTGTGACCTCTGGAGGGGGCGGGGTGTGTGTGGCC 2440
Dh      952  CysPheGlyTyrLeuThrLysGlnLeuMetGlyLeuAlaGlyIaIaGlyIleValLeuAla 971
Qy      2441  CTGGAGGAGGAGCAATGACTTGACCGGCACATCTGTGATGCTGTGAGTCTGAGTCTGGGCT 2500
Dh      972  LeuGluGlyGlyHnAspLeuThrAlaIleCysAspAlaSerGluAlaCysValSerAla 991
Qy      2501  CTGCTCAATGTAAAGCTGTGCAGCCCTTGTGATGAGGCAAGTCTTGACAGCAAAAGCCCAATC 2560
Dh      992  LeuLeuGlyAsnGlyLeuAspProLeuProGluLysValLeuGlnGlnArgProAsnAla 1011
Qy      2561  AAGCAGTGGCCACGCTAGAGAAAGTCAATCGATCCAGAGCAAACTGAGCTGTGTG 2620
Dh      1012  AsnIaValaIaArgSerMetGluLysValMetGluIleHnSerLysTyrTrpArgCysLeu 1031
Qy      2621  CAGAAGTGGCGCGTGTGTGGCGCGGCTCTGGAGGGGGCCAAAGCAAGTGAACGAA 2680
Dh      1032  GlnArgThrThrSerThrAlaGlyArgSerLeuIleGluIaIaGlnThrCysGluAsnGlu 1051
Qy      2681  GAAGCCGGAAT-GTGAAGCGCATGGGCTGTGTGTGTGGGGGCGGCAAGCCCAAGT 2739
Dh      1052  GlnIaGluThrValThrIleMetAlaSerLeuSerValGlyValLysProAlaGlu--- 1070
Qy      2740  GCGGCAAGCCCGGGAACAGAGCCCAAGCGGCAAGAGAGCCATGAGACAGAGCTTGGC 2799
Dh      1071  -----LysArgProAspGlnGluProMetGluGlnGluProPro 1083
Qy      2800  CTG 2802
Dh      1084  Leu 1084

RESULT 6
US-09-637-145-2
; Sequence 2, Application US/09637145
; Patent No. 6673587
; GENERAL INFORMATION:
; APPLICANT: EVANS, RONALD M.
; APPLICANT: KAO, HUNG-YING
; APPLICANT: DOWNS, MICHAEL
; APPLICANT: ORDENTLICH, PETER
; TITLE OF INVENTION: NOVEL HISTONE DEACETYLASE, AND USES THEREFOR
; FILE REFERENCE: SAKK3000

```

```

CURRENT APPLICATION NUMBER: US/09/637,145
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 938
TYPE: PRF
ORGANISM: Mus sp.
US-09-637-145-2

Alignment Scores:
Pred. No.: 5,59e-111 Length: 938
Score: 1773.00 Matches: 422
Percent Similarity: 54.79% Conservative: 110
Best Local Similarity: 43.46% Mismatches: 250
Query Match: 33.16% Indels: 190
DB: 4 Gaps: 24

US-09-502-945-2 (1-2885) x US-09-637-145-2 (1-938)

QY 2 GAATTTCCTTTGTGCAAGTCAAAAGAGCCCAACAGAGGCGGCTTCACCATTCCTCCCA 61
DB 114 GUAUUA11LeuUeUySeUg1nG1nA1a1eUg1uAgtHrVAlH1aPSeUSeUPro 133
QY 62 CAGCAGCC-----AAATCTGGGAGCCCAACAGCTTCCTTG 100
DB 134 Ser1LeProUyHrYHrThLeUg1uPro1eUyHrH1ng1uG1yAla1a1aUySeUVal1eU 155
QY 101 GACCAAGATTCCCTCCCAAGAGGAGCCCTCGGAGAGCTCCCTCTCAAACTGCT 160
DB 154 SeUSeUPro1eUPro1eUa1ProSeU1eUProH1ng1uPro1ProG1uH1S----- 170
QY 161 TTGCTGGGCGCTTACGACAGTGCAGACGACTTCCCTCCGCAAAAGCTTGAACCC 220
DB 171 -----PhePro1eUa1g1yThrValSeUg1uPro 180
QY 221 AACTGAAAGTGGTTCAAGGCTAAACAGAAAGTGGCTGAGCCGGAAGAGAGTCCCTC 280
DB 181 ASh1eU1ySeUyHrYHrYHrYSeUPro1yS--UySeU1eUg1uA1g1yUyAaPSeU1eU 195
QY 281 CTGGGTGCAGAGATGGAGCTGTTATTAGACACTTAAAGAAAGAGTGTGATGATGACA 344
DB 200 LeUa1g1ySeU1eUSeU1aPro-----ProSeU1eUa1g1a1g1uPro1a1aU1Th1eU 217
QY 341 GATGCGGAGCTGGGAGCTGTCCGTGTGTAAACAGAGGAGCCGAGCTCGGCGCCAGCTT 400
DB 218 G1YHrSeUSeUProSeUSeUSeU-----SeUThrPro1a1SeUg1UySeUSeU 234
QY 401 CCACAGCTCCCAACAGACACATCCGTAGAAATGGCTTTAATGAGTCAGTCCCAATC 460
DB 235 Pro1a1aPSeU-----G1uH1aG1y----- 241
QY 461 CCACAGATGCTCCCTACAGACCGAGGCGCTCCCTGACAGAGTCCCAACAGTTC 520
DB 241 ----- 241
QY 521 AGCTCTACAGCTCTCTTCTGCGCAACATCTCTAGGAGTGCAGAGCCAGCTCACT 580
DB 242 -----Pro1a1Pro1a1eUg1ySeUg1Ua1a1aPSeU1aPSeU1aPSeU1aPSeU 253
QY 581 GTACCAACTCAACCTCACTGCTCCCGGAAG----- 613
DB 254 ---ArgaUgThH1SeUTh1eUg1UyPro1a1g1UyPro1a1g1UyAaPSeU1a1a 272
QY 614 ---CTGTGCACACAGAGAGGCGCAAGAGGAGCGGCTCCAGTCCCTCGGAGAGGAGG 670
DB 273 Pro1eU1eU1HrYHrYSeU1eUg1uPro1G1uA1a-----G1yG1y 286
QY 671 ACCTGACCGGCAAGTTCATGACACATCTTATCTTGAGTGCCTGCTGGAGCTGGA 730
DB 287 Th1eU----- 288
QY 731 CTGAGAGGCGAGAGAGCCCAACGAGGAGATGCTCCCTGTCAGACATGTCCTTGTCTG 790

```



```

Db      289 -----ProSerArgLeuGlnProIleLeuLeu 298
Qy      791 GAGCAGGCGCCGGAGCAGACGACCCCTCATGTGCTG-----CCACTC 832
Db      299 AspProSerValSerHisAlaProLeuTrpThrValProGlyLeuGlyProLeuProPhe 318
Qy      833 CACGGCAGTCCCCCACTAGTACGGGTGAACGTGTGGCCACGACATGCGGACGTAGGC 892
Db      319 HisPheAlaTrnProLeuLeuThrThrGlnArgLeuSerGlySer----- 333
Qy      893 AAGCTCCCGGCGAGTGGCCCTTGAGCCGACATCTACGCTCACCCTGCGGACAGTCCC 952
Db      334 -----GlyLeuHisArgProLeuAsnArgThrArgSerGluProLeuProProSerAla 351
Qy      953 CAGGCGCTGAGAGCGGTGCATGACGACAACAGACGACGTCCTCGAGGAAGCAGAG 1012
Db      352 ThrAlaSerProLeuLeuAlaProLeuGlnProArgGlnAspArgLeu----- 367
Qy      1013 CACGACGAGCTACAGCTGGGCGAAGATCTTCACCAAGACAGGGAGCTGCCGACGAGCCC 1072
Db      368 LysProHisValGlnLeuIleLysProAlaIleSerProProGlnArgProAlaLysPro 387
Qy      1073 ACCACCCACCTTGAGAGACAGACAGAGAGAGCTGACGAGACGACGAGGCTTGCGGG 1132
Db      388 SerGluLysProArgLeuArgGlnIleProSerAlaGluAspLeuGluThr--AspGly 407
Qy      1133 GAGGAGAGCCTACACATGCCCCGGAGGGGCTC---CACAGAGGTGAGACACACAGAA 1189
Db      407 LysIleValAlaGlyProMetAlaAsnAspGlyLeuGlnHisArgGln-----SerIle 424
Qy      1190 GACCTGAGAGACAGAGACGAGAAAGAGATGGAGAGAGAGAGAGATTCATCCAGTT 1249
Db      424 ArgIleProProGluGluArgGly--SerIleSerLeuGlnGlnHisGlnIleValProPro 443
Qy      1250 AAGACGAGAGAGGCGAGAGCTGTGCTGAGAGAGGGCCGACTTGACGAGAGCTGTGCT 1309
Db      444 TrpGluGlnGlnHisLeuAlaGlyArg-----LeuSerGlnGlySerPro 458
Qy      1310 GGAATACAAAATGTTTCTCAGATGCCAACCCGCTGCACCTTGACAGGTGTACCAAGC 1369
Db      459 GlyAspSerValLeu----- 463
Qy      1370 CCCCCTCAGCTGCGCACTGTGCCCCACCAAGCCCTGGCCGTACCCCATCTCCCTGCT 1429
Db      464 ---IleProLeuAlaGlnValGlyHisArgProLeuSerThrArgIleSerSerProAla 482
Qy      1430 GCCCTGGGGGGCATGAAGAAACCCCCACAGACCAACCGCTC----- 1468
Db      483 AlaProValSerMetLeuSerPro-----GluProThrCysGlnThrGlnValLeuAsn 500
Qy      1469 ---AAGACCTCTTTCACCAACAAGTGTGTCTACGACCGTTCAAGCCAAAGCCAGTGC 1525
Db      501 SerSerGluThrProAlaTrnGlyLeuValTyrTrpAspSerValMetLeuLysHisGlnCys 520
Qy      1526 ATGTGGCGGAACAACACACTGTCACCTGACATGCTGGCCGATCCGACATCTGTGTC 1585
Db      521 SerCysGlyAspAspSerLysHisProGluHisAlaGlyArgIleGlnSerIleTrpSer 540
Qy      1586 CCGCTGACAGAGACMGCGCTGCTTACGAGTGCAGCGAGTCCGAGGTCCGAAAGCCAG 1645
Db      541 ArgLeuGlnGlnLysArgGlyLeuArgSerGlnCysGluLysLeuArgGlyArgLysAlaSer 560
Qy      1646 CTGAGTGAAGATTCACAGACAGTGCATGTGATACCAACACCTGTCTATGGGACAGTCCC 1705
Db      561 LeuGluGlnLysLeuSerValHisSerGluArgHisValIleLeuLysTrpGlyTrnAspPro 580
Qy      1706 CTCACACCGCAGAGTACAGACAGAGATGTGCTCGTCCATCCAGCCGAGAGATGTAT 1765
Db      581 LeuSerArgTrpLeuLysLeuAspAsnGlyLysLeuThrGlyLeuLeuAlaGlnHisArgTrpPhe 600
Qy      1766 GCTGTGCTGCTTGTGTGGGGCATCGGGGTGACAGTGCACCGTGTGAATGAGATGCAC 1825

```

```

Db      601 ValMetLeuProCysGlyGlyValGlyValAspThrAspThrIleTrpAsnGluLeuHis 620
Qy      1826 TCCCTCAGTGTGTGGCATGAGAGTGGCTGCTGCTGCTGACGCTTCAAGGTGCT 1885
Db      621 SerSerAsnAlaAlaArgTrpAlaAlaGlySerValThrAspLeuAlaPheLysValAla 640
Qy      1886 GCAGAGAGCTCAAGAAATGATTTGGCATATCCGCGCCCGACAGACACACCGCGAGAA 1945
Db      641 SerArgGluLeuLysAsnGlyPheAlaValAlaArgProProGlyHisHisAlaAspHis 660
Qy      1946 TCCACGCCATGGAGATTTCTTCTTCACTGTGTAGCCATCACCGCAAAATCCTACAG 2005
Db      661 SerThrAlaMetGlyPheCysPhePheAsnSerValAlaIleAlaCysArgGlnLeuGln 680
Qy      2006 CAGAAAGTTGAACGTGGGACAGGCTCATGCTGATGAGACATTCACCATGGCAATGCG 2065
Db      681 GlnHisGlyLysAlaAspLysIleLeuIleValAspTrpAspValHisHisGlyAsnGly 700
Qy      2066 ACCGACAGGCGCTTTCACATGACCCCTGTGCTGTACATCTTCTGCATGCTATGAC 2125
Db      701 ThrGlnGlnThrPheTyrGlnAspProSerValLeuTyrIleSerLeuHisArgHisAsp 720
Qy      2126 AACGGAACTTCTTTCACAGCTTCTGGGGCTCCCTGAAGAGATTTGTGTGAGACCAAGCCG 2185
Db      721 AspGlyAsnPhePheProGlySerGlyAlaValAlaAspGluValGlyThrAlaSerGlyGlu 740
Qy      2186 GGGTACATGTGAACGTGGCATGACAGAGAGGTGTGACCCCGCATTTGAGACGTTGAG 2245
Db      741 GlyPheAsnValAsnValAlaTrpAlaGlyGlyLeuAspProPheMetGlyAspProGlu 760
Qy      2246 TACCTTACAGCCTTCACAGACAGTGTGATGCCATTTGCCACGAGTTCTCACCTGATGTG 2305
Db      761 TyrLeuAlaAlaPheArgIleValValMetProIleAlaArgGluPheAlaProAspLeu 780
Qy      2306 GTCTTGTCTCCGCGGGTTTGATGTCTGTGAAGACATCTGTCTCTGCTGGGTGCTAC 2365
Db      781 ValLeuValSerAlaGlyPheAspAlaAlaGluGlyHisProAlaProLeuGluGlyTyr 800
Qy      2366 TCTGTACCGCCAGATGTTTGGCCACTTGACACGAGCAGCTGATGACCTGGCAGGAGGCG 2425
Db      801 HisValSerAlaLysCysPheGlyTyrMetThrGlnMetLeuMetLeuAlaGlyGly 820
Qy      2426 CCGGTGTGTCGCGCTGAGAGGAGGCGCATGACTTGACCCGCAATCTGTGATGCTTGA 2485
Db      821 AlaValValLeuAlaLeuGluGlyGlyHisAspLeuThrAlaIleCysAspAlaSerGlu 840
Qy      2486 GCTTGTGTCTCGGCTTGTCTCACTGTAAAGCTGTGACGCTTGTGATGAGCAGCTTTGCGAG 2545
Db      841 AlaCysValAlaAlaLeuLeuGlyAsnLysValAspProLeuSerGluLysSerTrpLys 860
Qy      2546 CAABAACCCCAACATCAAGCGAGGCGCATGAGAAAGTCAAGATCCAGACGACAA 2605
Db      861 GlnLysProAsnMetSerAlaIleArgSerLeuGluAlaValAlaArgValHisAspGly 880
Qy      2606 CACTGAGCTGTGTGACAGAGTTCCGCGC-----TGTGTGCGGCGGCTCCCT 2652
Db      881 TyrTrpGlyCysMetGlnArgLeuAlaSerCysProAspSerTrpLeuProArgValPro 900
Qy      2653 GCGAGGGGCGCCAAAGCAGGTGAGACCGAAGACCGAAAGTGAAGCCCATGTGCTGTGCTG 2712
Db      901 GlyAla-----AspAlaGluValGluAlaValAlaThrAlaLeuAlaSerLeu 915
Qy      2713 TTGTGTGGGG-----GCCGAACAGGCCCAAGCTGCGGACCGCGGAAACAGCCCGCAG 2766
Db      916 SerValGlyIleLeuAlaGluAsp-----Arg 924
Qy      2767 CCGGACAGAGAGCCCATGAGCAGAG 2793
Db      925 ProSerGluArgLeuValGluGluGlu 933

```

RESULT 7  
 US-09-644-827B-8  
 ; Sequence 8, Application US/09644827B

```
/ Patent No. 6762283
/ GENERAL INFORMATION:
/ APPLICANT: WALLACH, David
/ APPLICANT: SCHUCHMANN, Marcus
/ APPLICANT: GONCHAROV, Tanya
/ TITLE OF INVENTION: Caspase-8 Interacting Proteins
/ FILE REFERENCE: WALLACH=26
/ CURRENT APPLICATION NUMBER: US/09/644,827B
/ CURRENT FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: 132105
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: 127721
/ PRIOR FILING DATE: 1998-12-24
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 8
/ LENGTH: 1200
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-644-827B-8

Alignment Scores:
Pred. No.: 1,07e-108 Length: 1200
Score: 1739.50 Matches: 423
Percent Similarity: 50.75% Conservative: 121
Best Local Similarity: 39.46% Mismatches: 239
Query Match: 32.54% Gaps: 26
DB: 4

US-09-502-945-2 (1-2885) x US-09-644-827B-8 (1-1200)
QY 21 CAAGAGAGCCCAACGAGGCGCTCAACATTCCTCCACAGCACC---CCAAATGCT 77
DB 174 GlnuRgThrValHisProAsnSerProGlyIleProIyRArgSerGlnGlyProCysSer 193
QY 78 GGGGAGCCCAACATGCTTTTGACCAAGATTCCTCCACAGGCGCCCTGCGA 137
DB 194 GlyGln-CysProCys-----SerValProThrProLeuylGlnProItrPhI 209
QY 138 GCGC-----TC 143
DB 209 sSerPheCysArgThrLeuGluProLeuGluThrGluGlyAlaThrArgSerMetLeuSe 229
QY 144 CCTTCCTCAACAGCTTCCTTCCTGCGG---CCCTACAGACGTGACAGAGCTTCCTCCCTCC 200
DB 229 r-SerPheLeuProProIalProSerLeuProSerAapProProGluHisPheProLeuA 249
QY 201 GCAAAACAGCTCTGAACCACTTGAAGTGCCTTCAAGCTAAACAGAGAGGTGCGT 260
DB 249 rGlySerThrValSerGluProAsnLeuylGlnArgIyRlybProIyS---LysSerLeuG 266
QY 261 AGCGAGAGACAGTCCCTCTCGCTGCGCAAGATGAGGACTGTATTATGACCTTTAAGA 320
DB 268 lUatRgArgIyAsnProLeuLeuArgIyGlnSerAlaPro-----ProSerLeuArgA 286
QY 321 AGAGAGCTGTGAGTACACAGGTGCCGCGCTGCGGCGCTGCTGCTGTAAACAGCGCAC 380
DB 286 rGArgProAlaGluThrLeuGlyAspSerSerProSerSerSer-----SerThrp 303
QY 381 CCGGCTCCGCGCCAGCTCTCCCAACAGCTCCACAGCACCAGCTGAGAAATGACTTTA 440
DB 303 rolaSerGlyCysSerSerProAsnAspSerGluHis----- 315
QY 441 CTGGCTCAGTCCCAACATCCCACTGAGATGCTCCTCAGACACCGACCCCTCTGCG 500
DB 316 --GlyProAsnProIleLeuGlySerGlnAlaLeuGlnGlyGlnArgLeuArgLeuGln 335
QY 501 ACAGCTCCCAACCACTGAGCTCTACAGCTGTCTCTCTGCGCAACATCCCTCCCTAG 560
DB 335 lUthrSerValAlaProPheAlaLeuProThrValSerLeuLeuProAlaIleThrLeuG 355
QY 561 GGCTGACGAGCCACGCTGACTGTACCAACATCAGACTCACTGCTCCCGCAAGCTGTGCA 620
DB 620
```

```
DB 355 lUeuProAla-----ProA 360
QY 621 CACAGCAGAGGCGGAGGAGGAGGCGCTCCAGTCCCTGCGGCGAGGGTGGACGCTGACCG 680
DB 360 laArgAlaAspSerAapArgArgThrHisProThrLeuGlyProAlaGlyProIleLeuG 380
QY 681 GCAAGTTCATGACACATCTCTTATTCCTGCTGCTGCTGCTGCGGCGCTGAGAGCGCG 740
DB 380 lUeuProHisIsthProLeuPheLeuProHis-----GlyLeuGluProGluAlaG 397
QY 741 ACAGGAGCCCCACAGGCGATGCTCTCTGCTGACAGATGCTGCTGCTGCTGAGAGCGCC 800
DB 397 lUyGlyThr-----LeuProSerArgLeuGlnProIleLeuLeuAspProSerG 414
QY 801 GGCAGCAGACCACTTCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 860
DB 414 lUeuHisAlaProLeuLeuThrValProGlyLeuGlyProLeuProPheHisPheAlaG 434
QY 861 AACGTGCGCCACAGACATCGGACGAGTGAAGCTCCGCGCGCATCGGCGCTGAGCC 920
DB 434 lUeuLeuMetThrThrGlnArgLeuSerGlySer---GlyLeuHisIsthProLeuSerA 453
QY 921 GCACTCAGTCTTACCGCTGCGCAAGTCCCAAGCTCCAGGCT----- 958
DB 453 rGThrArgSerGluProLeuProProSerAaThrAlaProProProGlyProMetG 473
QY 959 -----CTGCAGCAGCTGTGATGCAACAAGACAGCAGCAGCTTCGTGGAAGCGA 1010
DB 473 lUProArgLeuGlnGlnLeu-----LysThrHisValGlnValIleLysArgSer- 489
QY 1011 AGCAGCAGAGCTACAGCTGGGCAAGTCTTCAACCAAGAGGAGAGCTCCAGGAGCAGC 1070
DB 490 -----AlaLysProSerGluLysProArg----- 497
QY 1071 CCAACCAACCTGAGAGACAGAGAGAGCTGACGAGCAGAGAGCTTCTCTG 1130
DB 497 ----- 497
QY 1131 GGGAGGAGCGCTGACCATGCCCCGGAGGCGCTCCACAGAGTGAAGACAGAGAG 1190
DB 498 -----LeuArgGlnI 501
QY 1191 ACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1250
DB 501 lUProSerAlaGluAspLeuGlnThrArgPly----- 511
QY 1251 AGGACGAGAGGCGAGAGTGT-----GCTGAGAGAGGCGCGCACTTGAAGAGCTTG 1304
DB 512 -----GlyGlyProGlyGlnValAlaAspArgGlyLeuGlnHisArgGlyLeuG 528
QY 1305 GTGCTGATTCAAAAAAGTCTTCTCAAGATGCCACAGCTGCAACCTTTGCAAGTGTAC 1364
DB 528 lUHisGlyGln-----ProGluAlaArgIyProAlaProLeuGln-----G 542
QY 1365 AACGCGCC----- 1372
DB 542 lUHisProGlnValLeuLeuThrPgluGlnGlnArgLeuAlaGlyArgLeuProArgGlyS 562
QY 1373 -----CTGAGCTGCGCACTGCTGCGCCCAACAGCTGAGCGCTGA 1412
DB 562 eThrGlyAspThrValLeuLeuProLeuAlaGlnGlyGlnHisArgProLeuSerArgA 582
QY 1413 CCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1453
DB 582 lUaGlnSerSerProAlaAlaProAlaSerLeuSerAlaProGluProAlaSerGlnAla 602
QY 1454 -----CCAGACCAACCGTCAAGACCTC---TTCAACCAAGTGTGTGT 1496
DB 602 rGValLeuSerSerSerGluThrProAlaArgThrLeuProPheThrThrGlyLeuIleT 622
QY 1497 ACAGCAGCTTATGTTAAAGACAGCTGATGTGCGGAGAACACAGCTGACAGCTTGTAC 1556
DB 622 yUAspSerValMetLeuLysGlnCysSerGlyLysAspSerAArgHisProGluI 642
```

```

QY 1557 ATGCTGGCCGGATCCAGAGCATCTGTGCTCCGGCTGCAGAGACAGCGCTTGATGCAAGT 1616
Db 642 1sa1aGlYArg11eGlnSer11eTrpSerArgLeuGlnGlnArgGlyLeuArgSerGlnC 662
QY 1617 GCGAGCGCAATCCGAGGCGGAAAGCCAGCTAGATGATGATCCAGACAGCTGATCTGGAAT 1676
Db 662 1ys1uCy5LeuArgGlyArgLysAlaSerLeuGlnGlnLeuGlnSerValHisSerGlnA 682
QY 1677 ACCACACCTGCTCTATGGAGCAGCATCCCTCAACCGGACAGACTAGACAGCAAGAGT 1736
Db 682 rgh1sVal1euleuTrpGlyThrAsnProLeuSerArgLeuLysLeuAspAsnGlyLysL 702
QY 1737 TGCCTGGTCCATCAGCCAGAGAAATGTATGCTGTGCTGCTGTGCGGCGATCGG- 1792
Db 702 eua1aGlyLeuLeu1aGlnArgMetPheValMetLeuProCysGlyGlyValGlyProL 722
QY 1792 ----- 1792
Db 722 eua1aThrLysSerAlaPheLeuAlaSerLeuAlaProThrValProGlnGlyLeuSerA 742
QY 1792 ----- 1792
Db 742 rglValSerTrpGlyLeuLysProProGlyProAsnProLysSerArgProAlaProC 762
QY 1792 ----- 1792
Db 762 1ysProTrpGlyProGlyArgGlyValGlyThrThrProLeuGlyProGlySerCysValL 782
QY 1793 ----- 1793
Db 782 1ysProTrpMetMetArgAlaLeuThrLeuAlaProGlnValAspThrAlaSerThr11eTrpA 802
QY 1815 ATGAGATGACACTGCTCCAGTGTGTGCGCATGGCAGTGGGCGCTGCTGAGCTGGGCT 1874
Db 802 snGlnLeuHisSerSerAsnAlaAlaArgTrpAlaAlaGlySerValThrAspLeuAlaP 822
QY 1875 TCAGAGTGGCTGCAGAGAGACTCAAGATGATTTGTCATCATCCGCGCCCGCCAGAGACC 1934
Db 822 he1ysValAlaSerArgGlnLeuLysAsnGlyPheAlaValAlaArgProProGlyHisH 842
QY 1935 ACCCGGAGGAATCCAGAGCATGCGATCTGCTCTTCACTGATCTGATCATCTCTGTC 1994
Db 842 1sa1aAspHisSerThrAlaMetGlyPheCysPhePheAsnSerValAla11eAlaCysA 862
QY 1995 AACTCTACAGACAGAGTTGAACGTGGCAAGGCTCATCTGATGAGACTGGAATTCACC 2054
Db 862 rglGlnLeuGlnGlnGlnSerLysAlaSerLys11eLeu11eValAspTrpAspValHisH 882
QY 2055 ATGGCAATGGCAATCCAGAGCGCTTCTACAAATGACCCCTGTGCTCTACATCTCTGTC 2114
Db 882 1saGlyAsnGlyThrGlnGlnThrPheTrpGlnAspProSerValLeuTrp11eSerLeuH 902
QY 2115 ATGGCTATGACAAAGGAACCTTCTTCCAGGCTCTGGGCGCTCCCGAAGAGATTGTGGAG 2174
Db 902 1saTrpHisAspAspArgLysAsnPhePheProGlySerGlyAlaValAspGlnValGlyAlaG 922
QY 2175 GACGACGGCGGGGTACAAATGTGAACGTGGCATGACAGAGGTGTGACCCCGCCCATTTG 2234
Db 922 1ysSerGlyGlnGlyPheAsnValAsnValAlaAlaTrpAlaGlyGlyLeuAspProPrometG 942
QY 2235 GAGACGTGAGTACTTTACAGCCTTCAGACAGTGTGATGCCCATGACTTCT 2294
Db 942 1ysAspProGlnTrpLysLeuAlaAlaPheArg11eVal11eValMetPro11eAlaArgGlnPheS 962
QY 2295 CACCTGATGTGCTTCTAGTCTCCGCGGCTTGTATGCTGTGTAAGACATCTGCTCTC 2354
Db 962 erProAspLeuValLeuValSer11aGlyPheAspAlaAlaGlnGlyHisProAlaProL 982
QY 2355 TGGGTGGCTACTGTGTCACCGCCAGATGTTTGGCACTTGACACGAGCATGTGACCC 2414
Db 982 euaGlyGlyTrpHisValSerAlaLysCysPheGlyTrpMetThrGlnGlnLeuMetAsnL 1002

```

```

QY 2415 TGGCAGGGGGCCGGGTGCTGCTGCGCTTGGAGAGAGCCCATGATCTTG 2474
Db 1002 eua1aGlyValAlaValAlaLeuAlaLeuGlnGlyGlyHisAspLeuThrAla11eCysA 1022
QY 2475 ATGCCCTGATAGCTGTGTCTGCGCTCTGCTCAGTGTAAAGCTGACGCTTGATGAG 2534
Db 1022 sPh1aSerGlnAlaCysValAlaAlaLeuLeuGlyLysAsnArgValaAspProLeuSerGlnG 1042
QY 2535 CAGTCTTGACGAAAAGCCCAATCAACGACAGTGGCCACGTTAGAGAAATCATGACA 2594
Db 1042 1uGlyTrpLysGlnLysProAsnLeuAsnAla11eArgSerLeuGlnAlaVal11eArgV 1062
QY 2595 TCCAGAGCAAAACACTGAGACTGTGTGCAGAAAGTTCGCCCTGTGCTGGCCGCTCCTGC 2654
Db 1062 11eHisSerLys----- 1065
QY 2655 GAGGGGCCAAGCAGGTGACCGAAGCCGAATGTGAACGCATGCGCTTGCTGT 2714
Db 1066 -----CysGlyAspGlyThrLeuAlaGlnLeu----- 1074
QY 2715 GGTGGGGGCGCAACAGGCCAAGCTGCGGACCGCGGAACACAGCCCGGACAG 2774
Db 1075 -----ArgLeuLysAspLeuGlyGlyThrLeuProHisArgGlyG 1088
QY 2775 GGAAGCCCATGAGACAGAGAGCTGCGCTGTGAC 2806
Db 1088 11eLeuGlnLysPheArgCysGlnProGlyAsp 1098

RESULT 8
US-09-644-827B-7
/ Sequence 7, Application US/09644827B
/ Patent No. 6762283
/ GENERAL INFORMATION:
/ APPLICANT: WALLACH, David
/ APPLICANT: SCHUCHMANN, Marcus
/ APPLICANT: GONCHAROV, Tanya
/ TITLE OF INVENTION: Caspase-8 Interacting Proteins
/ FILE REFERENCE: WALLACH=26
/ CURRENT APPLICATION NUMBER: US/09/644, 827B
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: 132105
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: 127721
/ PRIOR FILING DATE: 1998-12-24
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 7
/ LENGTH: 1428
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-644-827B-7

Alignment Scores:
Pred. No.: 1,12e-108 Length: 1428
Score: 1739.50 Matches: 422
Percent Similarity: 50.75% Conservative: 121
Best Local Similarity: 39.46% Mismatches: 239
Query Match: 32.54% Indels: 289
DB: 4 Gaps: 26

US-09-502-945-2 (1-2885) x US-09-644-827B-7 (1-1428)
QY 21 CAAAGAGCCCAACAGGCGGCTGCAACATTCCTCCACAGACAC---CCAAATGCT 77
Db 400 G1uArgThrValHisProAsnSerProGlyLysProTyArgSerGlnGlyProCysSer 419
QY 78 GGGAGCCCAACATGCTTCTTTGACCAAGATTTCCCTCCCAAGCGGCGCCCTTGGA 137
Db 420 G1yGln-CysProCys-----SerValProThrProLeuLysGlnProTrpH 435
QY 138 CGCG----- -TC 143
Db 435 sSerPheCysArgThrLeuGlnProLeuGlnThrGlnGlyAlaThrArgSerMetLeuSe 455

```

QY	144	CCCTCTCAAAATGCTGTTGGCTGGG---CCCTACGACAGTGCAGACATTTCCCTCC	200
Db	455	T-SerPheLeuProValProValProSerLeuProSerAaPProProGluIvPheProLeuA	475
QY	201	GCAAAACAGCTCTGAAACCAATTGAAGTGCCTTCAAGCTAAACAGAAAGTGCCTG	260
Db	475	rgLyvThValSerCiuProAheLeuIvPheAArgTyLyvProLyv---LysSerLeuG	494
QY	261	AGCGGAGAACAGTCCCTCTGCTGCCTCCGCAAGATGGAGCTGTATTAGCACTTTAAGA	320
Db	494	IuArgTyLyvAaAaPProLeuLeuArgLyvGIuSerAlaPro-----ProSerLeuAaGA	512
QY	321	AGAGAGCTGTGAGATCAAGATGCGGGGCTGGGGCGCTGCCTGCTGTGTAAACGCGAC	380
Db	512	rgArgProAlaGIuThrLeuIvAaPserSerProSerSerSer-----SerThrP	529
QY	381	CCGGCTCCGGGCCCCAGCTCTTCCCAACAGCTCCACAGACCAATGCTGAGAATGGCTTTA	440
Db	529	roAlaSerGIvCyuSerSerProAaAaPserCuihIs-----	541
QY	441	CTGGGTACGTCCCAACATCCCAATGAGATGCTCCCTCAGACACAGACCTCCCTCTGG	500
Db	542	--GIvProAaPProIvLeuGIuSerGIvAlaLeuGIvGIuThArgLeuArgLeuGIuG	561
QY	501	ACAGCTCCCAACCAAGTTTACAGCTCTACAGCTCTCTTCTGCGCCAACTTCCCTAG	560
Db	561	IuThrSerValAlaPheProAaLeuPProThrValSerLeuLeuProAlaIleThrLeuG	581
QY	561	GGCTGCAGAGCCAGGCTACTGTACCAACTACACACTACGTGCTCCCGAAAGCTGTGA	620
Db	581	IyLeuProAla-----ProA	586
QY	621	CACAGCAGAGAGCCAGAGAGGCGCTCCAGCTCCGCGAGGATGGACAGCTGACCG	680
Db	586	IaArgAlaAaPserAaPArgThrIvPProThrLeuGIvProArgGIvProIleLeuG	606
QY	681	GCAGTTTCATGACACATCTCTATTCTGTGCTGCTGCTGCGCGTGGCACTGAAGGCG	740
Db	606	IySerProhIvThrProLeuPheLeuProhIs-----GIvLeuGIuProGIuAlaG	623
QY	741	ACGGGAGCCCCAGGGGATGCTCCCTCCGCTGCGAGATGCTGTGTGAGACAGGCCC	800
Db	623	IyGIuThr-----LeuProSerAlaArgLeuGIuPProIvLeuLeuLeuAaPProSerG	640
QY	801	GCGACAGAGAGCACTCATGCTGTGTCACCTTSCACGGGCACTGCCACTAGTGAAGGTG	860
Db	640	IySerhIvAlaPProLeuLeuThrAlvProGIvLeuGIvProLeuPProhIvAaPheAlaG	660
QY	861	AACTGTGTGCAACCAAGATGCGGAAGGTGAAGCAAGCTCCCGGCGATGTGGCCCTGAAC	920
Db	660	IuSerLeuMetThrThrGIuThArgLeuSerGIySer---GIvLeuThIvPProLeuSerA	679
QY	921	GCACTCAGTCTCCACCGCTGCCGAGATGCCCAAGGCC-----	958
Db	679	rgThrArgSerGIuProLeuPProPProSerAlaThrAlaPProPProProGIvProMetG	699
QY	959	-----CTGCAGACAGCTGTGCATGCAACAACAGCAACAGCAAGTCTCTGAGAGACAGA	1010
Db	699	IuProArgLeuGIuGIuLeu-----LysThrIvAaGIuValIvIleuArgSer-	715
QY	1011	AGCAGCAGACACTACAGTGGGCAAGATCTTCACCAADAACAGGGGAGTGGCGAGCG	1070
Db	716	-----AlaLyvPProSerGIuLyvProArg-----	723
QY	1071	CCACACCCCACTGAGAGACAGAGAGAGCTGACCGACAGAGAGGCTTGTCTGG	1130
Db	723	-----	723
QY	1131	GGAGAGGAGCCCTGACATGCCCCGGAGGGGCTCCACAGAAATGAGACACAGAAAG	1190
Db	724	-----LeuArgGIuI	727

QY	1191	ACCTGAGAGAGAGAGAGAGAGAGATGGGAGAGAGAGAGAGAGAGATTCAGATCCAGGTTA	1250
Db	727	leProSerAlaGlnAspLeuGlnThrAspGly	737
QY	1251	AGGACGAGAGAGAGAGAGAGTGT-----GCTGAGAGAGGCGCCAGCTTGAGAGAGCCTG	1304
Db	738	-----GlyGlyProGlyGlnValValAspAspGlyLeuGlnHisArgGlyLeuG	754
QY	1305	GTGCTGGATACAAAAAAGCTGTTCTCAGATGCGCCACCGCTGCAACCTTTTGAGGTGTAAC	1364
Db	754	lyHisGlyGln-----ProGlnAlaAspGlyProAlaProLeuGln-----G	768
QY	1365	AAGCGCCC-----	1372
Db	768	lnHisProGlnValLeuLeuThrPheGlnGlnAspLeuAlaGlyAspLeuProAlaArgGlyS	788
QY	1373	-----CTGAGCCTGGGCACTGTGTGCCCCACCAAGAGCCCTGGAGGCGGTA	1412
Db	788	erThrGlyAspThrValLeuLeuProLeuAlaGlnGlyGlyHisArgProLeuSerAspArg	808
QY	1413	CCCAATCCTCCCTGCTGTCGCCCCGTGGGGGACATGAAGAACCC-----	1453
Db	808	laGlnSerSerProAlaAlaProAlaSerLeuSerAlaProGlnProAlaSerGlnAla	828
QY	1454	-----CCAGACCAACCCGCTCAAGACACTC--TTGACCAACAAGTGTGCT	1496
Db	828	rgValLeuSerSerSerGlnThrProAlaArgThrProPheThrThrGlyLeuLeu	848
QY	1497	ACGACAGCTCATCTTAAGACACAGAGGCATGTGCGGGAAACACACAGCTGACCTTGAGC	1556
Db	848	yrAspSerValMetLeuLeuYehiSeGlnCySerCySgIlyAspAsnSerArgHisProGlnH	868
QY	1557	ATGCTGGCCGGATCCAGAGCATCTGTGTCGGGCTGCAGAGACAGAGCCTGCTTAGACAT	1616
Db	868	leAlaGlyArgIleGlnSerIleThrSerArgLeuGlnGlnArgGlyLeuArgSerGlnC	888
QY	1617	GCGAGCGGATCCGAGGTGCGCAACCCAGCAGCTAGATGAGATCCAGACAGCTGACTTGAA	1676
Db	888	ysGlnCyValLeuArgGlyAspGlyValSerLeuGlnGlnGlnSerValHisSerGlnA	908
QY	1677	ACCAACCCGCTCTATAGGAGCCAGTCCCTCCACCGGAGAGACTGTAGACAGAAAGT	1736
Db	908	rgHisValLeuLeuThrGlyThrAsnProLeuSerArgLeuValLeuAspAsnGlyIlySL	928
QY	1737	TGCTCGGCTCCATCAGCAGAGAAATGATGTATGCTGCTGCTGCTTGTGGGGGAGCTGGG---	1792
Db	928	euaIaGlyLeuLeuAlaGlnArgMetPheValMetLeuProCySgIyGlyValGlyProL	948
QY	1792	-----	1792
Db	948	euaIaThrLeuSerAlaPheLeuAlaSerLeuAlaProThrValProGlnGlyLeuSerA	968
QY	1792	-----	1792
Db	968	rgValSerTrpGlyLeuIlySerProProGlyProAsnProIlySerAspProAlaProC	988
QY	1792	-----	1792
Db	988	ysProTrpGlyProGlyAspGlyValGlyValGlyThrThrProLeuGlyProGlySerCyValL	1008
QY	1793	-----GTGACAGTGACACCGGTGGA	1814
Db	1008	ysProTrpMetLeuArgAlaLeuThrThrLeuAlaProGlnValAlaThrThrIleTrpA	1028
QY	1815	ATGAGATGACATCTCTCCAGTGTGTGTGGCATGGCAGTGGGCTGCTGCTGAGCTGGCCT	1874
Db	1028	snGlnLeuHisSerSerAspHisAlaIaArgTrpAlaIaGlySerValThrAspLeuAlaP	1048
QY	1875	TCAAGGTGGCTGAGAGAGCTCAAGAAATGATTTGCAATCATCCGCGCCCGACAGACACC	1934
Db	1048	heIlyValAlaSerArgGlnLeuLeuYahsnGlyPheAlaValAlaIlyngProProGlyHisH	1068
QY	1935	ACGCGGAGAAATCCACAGCCATGGGAATTCGCTTTCACCTCTGTAGCATCCGCA	1994

```

Db      1068  isAlaAspHisSerThrAlaMetGlyPheCysPhePheAsnSerValAlaIleAlaCysA 1088
Qy      1995  AACCTCCACAGACAGAGTGAAGCTGGAGGCCATCGAGGATGGAGACATCCACC 2054
Db      1088  rglInLeuGlnGlnGlnSerLysLeuAlaSerLysIleLeuIleValAspTyrPaspValHisH 1108
Qy      2055  ATGGCAATGGACACCCAGACAGCGCTTCTACATGACCCCTGTGCTCTACATCTCTGCG 2114
Db      1108  isglYenGlnGlnGlnGlnThrPheTyrGlnAspProSerValLeuTyrIleSerLeuH 1128
Qy      2115  ATGGCTATGACAAACGGGAACCTTTCTTCCAGGCTCTGGGGCTCTGGAAGAGTTGGTGAG 2174
Db      1128  isArgHisAspAspGlyAsnPhePheProGlySerGlyAlaValAspGlyValGlyAlaG 1148
Qy      2175  GACGAGCGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2234
Db      1148  lyserGlyGlyGlyGlyPheAsnValAsnValAlaTyrAlaGlyGlyLeuAspProPheMet 1168
Qy      2235  GAGACGTGAGAGTACCTTACAGCCTTACAGACAGTGTGATGATGATGATGATGATGATG 2294
Db      1168  lyAspProGlyGlyGlyLeuAlaAlaPheArgIleValValMetProIleAlaArgGlnPheS 1188
Qy      2295  CACCTGATGTGCTTCCTGATGCTCCGCGGCTTGTGATGCTGTGATGATGATGATGATG 2354
Db      1188  expProAspLeuValLeuValSerAlaGlyPheAspAlaAlaGlyGlyHisProlAbProl 1208
Qy      2355  TGGGTGCTACTTGTGATCGCGGATGTTTGGACCTTACAGACAGGATGATGATGATGATG 2414
Db      1208  euGlyGlyTyrHisValSerAlaLysCysPheGlyTyrMetThrGlnGlnMetAsnL 1228
Qy      2415  TGGCAGGGGGCCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2474
Db      1228  euAlaGlyGlyAlaValValLeuAlaLeuGlnGlyGlyHisAspLeuThrAlaIleCysA 1248
Qy      2475  ATGCTCTGAAAGCTTGTGTCTCGGCTCTGCTCAAGTGAAGCTGACGCTTGGATGAGG 2534
Db      1248  sPalaSerGlnAlaCysValAlaAlaLeuLeuGlyAsnArgValAspProLeuSerGlyG 1268
Qy      2535  CAGCTTGACGACAAAGCCCAACATCAAGCAGAGGCGCCGCTTACAGAAAGTCAAGAGA 2594
Db      1268  luGlyTyrPlyGlnLysPheAsnLeuAsnAlaIleArgSerLeuGlnAlaValIleArgV 1288
Qy      2595  TCCAGACCAAAACATGAGCTGTGTGCAAGTTCGCGCTGTGCTGGCGCGCTGCTGCG 2654
Db      1288  alHisSerLys----- 1291
Qy      2655  GAGGGGCGCCAAAGAGGTGAGACCGAAGACCCGAATGTGAAGCCATGGCCTTGGCTTT 2714
Db      1292  -----CysGlyAspGlyThrLeuAlaGlnLeu----- 1300
Qy      2715  GGTGGGGGGCGGAACAGCCCAAGCTGCGGAGCGCCCGGGAACACAGCCCGAGCGCGAGA 2774
Db      1301  -----ArgLeuLysAspLeuGlyGlyThrLeuProHisArgGlyG 1314
Qy      2775  GAGGCCATGAGAGCGAGGAGCTGCGCTGTGAC 2806
Db      1314  InIleLeuGlyPheArgCysGlnProGlyAsp 1324

```

```

; PRIOR APPLICATION NUMBER: 127721
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-644-827B-6

Alignment Scores:
Pred. No.: 1,316-97      Length: 574
Score: 1573.00          Matches: 317
Percent Similarity: 68.65%      Conservative: 75
Best Local Similarity: 55.52%      Mismatches: 109
Query Match: 29.42%      Indels: 71
DB: 4                      Gaps: 9

US-09-502-945-2 (1-2885) x US-09-644-827B-6 (1-574)
Qy      1202  GAGACGAGAGAGAGATGAGGAGAGAGAGAGATTCACAGTTAAGACGAGAGAG 1261
Db      29  GluAspLeuGlnThrAspGly----- 35
Qy      1262  GCGGAGAGTGGT-----CCTGAGAGAGGCGCCGACTTGAAGAGCCTGTGCTGATAC 1315
Db      36  GlyGlyProGlyGlnValValAspAspGlyLeuGlnHisArgGlyLeuGlyHisGlyGln 55
Qy      1316  AAAAATGTTCTGCATGATGCCCAACCGCTGCAACCTTGTACAGGTGTAACGAGCGCC 1372
Db      56  -----ProGlnAlaArgGlyProAlaProLeuGln-----GlnHisProGln 69
Qy      1372  ----- 1372
Db      70  ValLeuLeuThrGlnGlnGlnArgLeuAlaGlyArgLeuProArgGlySerThrGlyAsp 89
Qy      1373  -----CTACGCTGGCCACTGTGCGCCACCAAGCCCTGGAGCCGTACCCAAATCTTC 1423
Db      90  ThrValLeuLeuProLeuAlaGlnGlyGlyHisArgProLeuSerArgAlaGlnSerSer 109
Qy      1424  CCGTGTGCGCCCGGGGGGCGAAGAACCC----- 1453
Db      110  ProAlaAlaProAlaSerLeuSerAlaProGlnProAlaSerGlnAlaArgValLeuSer 129
Qy      1454  ---CCAGACCAACCCCTCAAGACCTC---TTCAACCAAGTGTGTGCTTACGACAGTTTC 1507
Db      130  SerSerGlnThrProAlaArgThrLeuProPheThrThrGlyLeuLeuLysSerVal 149
Qy      1508  ATCTTAAGCAGCAGTGCATGTGCGGGAACACACAGTGCACCTTGAGCATGTGGCCGG 1567
Db      150  MetLeuLysHisGlnCysSerCysGlyAspAsnSerArgHisProGlnHisAlaGlyArg 169
Qy      1568  ATCCAGAGCATCGTGTCCGCGCGCGAGAGACAGCGCTCTTACGAAGTGGCGAGCGATC 1627
Db      170  IleGlnSerIleTyrSerArgLeuGlnGlnGlyGlyLeuArgSerGlnCysGlyLeu 189
Qy      1628  CGAGTTCGAAAGCCAGCTAGTGAATGATGATGATGATGATGATGATGATGATGATGATG 1687
Db      190  ArgGlyArgGlyAspAspLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG 209
Qy      1688  CTCTATGGACACAGTCCCTCAACCGGAGAAAGTGAACAGCAAGAAAGTTGCTGGTCCC 1747
Db      210  LeuTyrGlyThrAsnProLeuSerArgLeuLysLeuAspAsnGlyLysLeuAlaGlyLeu 229
Qy      1748  ATACGACAGAAAGTATGATCTGTGCGCTTGTGGGGGATCGGGGTGAGCAGTGAACCC 1807
Db      230  LeuAlaGlnArgIleThrValMetLeuProCysGlyGlyValGlyValAlaAspThrAspThr 249
Qy      1808  GTGTGAATGATGATGATCTCTCACTGTGTCGCGCATGCGCATGCGCATGCGCTGCTGAG 1867
Db      250  IleTyrAsnGlnLeuHisSerSerAsnAlaAlaArgTyrAlaAlaGlySerValThrAsp 269
Qy      1868  CTGGCTTCAAGGTGCTGCAGAGAGCTCAAGAAATGATTGTCATTCGCGCCCA 1927

```

```

Db      270 LeuAlaheIyValAlaSerArgGluLeuIysnGlyPheAlaValAlaArgProPro 289
Qy      1928 GGAACACACCCGAGAAATCCACAGCATGGGATTCCTTCTTCACTCTGTGACATC 1997
Db      290 GlyHieHieAlaSerPheSerThrAlaMetClyPheCysPhePheAsnSerValAlaIle 309
Qy      1988 ACCGAAATCTCTACAGAGAAAGTTGAACGTGGGACAGGCTCATCTGTGATGGGAC 2047
Db      310 AlaCysArgGlnLeuGlnGlnGlnSerLysAlaSerLysIleLeuAlaAspTTPAsp 329
Qy      2048 ATTCAACCATGGCAATGGCACCCAGCAGCGCTTCTTCAATGACCCCTGTGCTTACATC 2107
Db      330 ValHieHieGlyAsnGlyThrGlnGlnThrPheTyrglnAspProSerValIleuTyIle 349
Qy      2108 TCTCTGATGCTATGACAAAGGAACTTCTTCCAGGCTCTGGGGCTCTGGAAGAGTT 2167
Db      350 SerLeuHieHieArgHieAspAspGlyAsnPhePheProGlySerGlyAlaValAspGluVal 369
Qy      2168 GGTGAGAGACACAGGCGTGGGATACATGTGACGTGGACATGACAGAGGTGTGACCCC 2227
Db      370 GlyAlaGlySerGlyGlyGlyPheAsnValAsnValAlaTTPAlaGlyGlyLeuAspPro 389
Qy      2228 CCCATTGAGACGTGAGTACCTTACAGCCTTACAGACAGTGTGATGCCATTGCCAC 2287
Db      390 ProMetClyAspProGlyTyrglnAlaAlaPheArgIleValValMetProIleAlaArg 409
Qy      2288 GAATTCCTCACTGATGCTGCTCTTCTGCTCCGCGGCTTGTGATGCTGTGAAGACATCTG 2347
Db      410 GluPheSerProAspLeuValIleValSerAlaGlyPheAspAlaAlaGlyGlyHiePro 429
Qy      2348 TCTCTCTGGGATGCTACTGCTGTGACCCGACAGATGTTTGGCCATGACAGGACAGCTG 2407
Db      430 AlaProLeuGlyGlyTyrglnAlaSerAlaLysCysPheGlyTyrglnGlnGlnLeu 449
Qy      2408 ATGACCTTGACAGGCGGCGCGGTGCTGCTGCTGACAGGAGGAGCCATGACCTGACCC 2467
Db      450 MetAsnLeuAlaGlyAlaValIleValLeuAlaLeuGlyGlyHieAspLeuThrAla 469
Qy      2468 ATCTGTGATCCCTCTGAAAGCTGTGTCTGCGCTGCTGCTGCTGAAAGCTGACCCCTTG 2527
Db      470 IleCysAspAlaSerGluAlaCysValAlaAlaLeuLeuGlyAsnArgValAspProLeu 489
Qy      2528 GATGAGGACATCTTGGACAAAGCCCAACATCAACAGCAGTGGCGCGCTGTGAGGAAGTC 2587
Db      490 SerGlnGlnGlyTyrglnGlyAsnProAsnLeuAsnSerIleArgSerLeuGluAlaVal 509
Qy      2588 ATCGAGATCCAGAAACACTGAGCTGTGTGACAGAGTTTCGCGCTGTGAGCGCG 2647
Db      510 IleArgValHieSerLysTyrglnGlyCysMetClnArgLeuAlaSerCysProAspSer 529
Qy      2648 TCCCTCGAGAGGCGCCAGACAGGTGAGACCGAAGACCGGAAT-GTGAAGCCCATGGCC 2706
Db      530 TrpValProArgValProGlyAlaAspLysGlnGluValAlaValThrAlaLeuAla 549
Qy      2707 TTCTGTGTGTGGGG-----GCCGAACAGGCCCAAGCTCGGAGCGCGGAACACAGC 2760
Db      550 SerLeuSerValGlyIleLeuAlaGluAsp----- 559
Qy      2761 CCCAGGCGGACAGAGACCCATGACAGAGAG 2793
Db      560 ---ArgProSerGlnGlnLeuValGlnGlnGlu 569

```

```

; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraParseFormatler Version 0.9
; SEQ ID NO 649
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)---(0)
; OTHER INFORMATION: Polypeptide Accession Number YNL021W
US-09-538-092-649

Alignment Scores:
Pred. No.: 4,56e-37 Length: 706
Score: 672.00 Matches: 162
Percent Similarity: 50.40% Conservative: 87
Best Local Similarity: 32.79% Mismatches: 165
Query Match: 12.57% Indels: 80
DB: Gaps: 15

US-09-502-945-2 (1-2885) x US-09-538-092-649 (1-706)
Qy      1235 GATTGCATCCAGTTTAAGACAGAGAGGCGAGAGTGTGCTGAGAGAGGCGCCGACTTG 1294
Db      2 AspSerValMetValIlyAspGluVal-----Leu 11
Qy      1295 GAGAGGCTGTGCTGATGATCAAAAATCTTCTCAAGTCCCAACCGCTGACACTTG 1354
Db      12 GluAsnProAspHieAspLeuLysArgLysLeuGlnGlnLeuLys----- 26
Qy      1355 CAGGTATCCAGAGCGCCCTCAGCTGCGCATGTGCCCAACAGCCCTGAGCGGTACC 1414
Db      27 -----GlnGlnGlnAsnSerLeuSerThr-----SerLysSer 38
Qy      1415 CAATCTCCCTCTGCTGCTGCTGAGGAGTGAAGACCCCAACCAACCCGTCAAGCAC 1474
Db      39 LysArgGlnValIleValProValCysMetProLysIleHieTyrglnProLeuLys--- 57
Qy      1475 CTCTTACCAACAGTGTGCTATGACAGCTGATGATTAAGACCAAGTGCATGTGCGGG 1534
Db      58 -----ThryLeuCysTyrglnAspValArgMetArgTyrglnAlaLysIlePheThr 74
Qy      1535 AAC-----ACACAGCTGACACCTGACATGCTGCGCGATGCCAGACATCTGG 1582
Db      75 SerTyrglnGlnTyrglnLeuAspProHieAspProGluAspProArgArgIleTyrglnIleTyrgln 94
Qy      1583 TCCCGCTGACAGACAGAGCTGCTTACGAG----- 1615
Db      95 LysIleLeuLeuGlnGlnGlnGlnLeuIleAsnAspProThrLeuSerGlyValAspAspLeu 114
Qy      1616 -----TGCAGAGGAGATCCGAGGTTCGAAAGCACAGCTGATGATGATGATGATGATG 1666
Db      115 GlyAspLeuMetLeuLysIleProValArgAlaAlaThrSerGlnGlnIleLeuGluVal 134
Qy      1667 CACTCTGAATACCAAC---ACCCTGCTTATGGAGCAGTCCCTCAACCGGACGAGAGTGA 1723
Db      135 HieThrLysGlnHieLeuGlnPheIleGlnSerThrGlnLysMetSerArgGlnGlnLeu 154
Qy      1724 -----GACACGACAAAGATTGCTCGGTCCCATCAGCCAGAAAGATGATGCTGTGCTGCT 1777
Db      155 LeuLysGlnThrGlnLys----- 160
Qy      1778 TGTGGGGGATGAGGGGTGACAGTGAACCGTGTGATGATGATGATGATGATGATGATGATG 1837
Db      161 -----GlyAspSerValTyrglnPheAsnAspSerTyrglnAlaSer 173
Qy      1838 GTGCGATGACAGTGTGCTGCTGCTGAGAGTGGCTTCAAGTGTGCTGACAGAGAGCTC 1897

```





```

Db      318 AlaleuGly-----CyProGluGlyGluMetGluValThrProAlaCyTyProHis 335
Qy      2393 TTGACGACGAGCGATGACCCCTTGCGAGGGGCGGGGTGTGTGCGCCCTGAGGAGGAGC 2452
Db      336 LeuLeuAnProLeuLeuAlaArgLeuAlaAspAlaArgValAlaValLeuGluGly 355
Qy      2453 CATGACTTACCCGCGATCTGTGATGCTGTGAAGCTTGTCTGGCTGCTGCTGAGTGA 2512
Db      356 TyrCyLeuAnPserLeuAlaGluGlyAlaAlaLeuThrLeuAspSerLeuGlyAsp 375
Qy      2513 AAGTCGAGCCCTTGATGAGGAGCGCTTGCGAGAAAGCCCAATCAACGAGTGGCC 2572
Db      376 ProCyProProLeuValGluThrVal-----ProLeuProArgAlaGluLeuAlaGln 393
Qy      2573 ACGTTAAGAAAGTCATCGATCCAGACGAACATCTGAGCTGTGGCG 2623
Db      394 AlaleuLeuSerCyAlaAlaValHisArgProHisThrPargCyLeuGln 410

RESULT 12
US-09-502-540-15627
; Sequence 15627, Application US/0902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15627
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-502-540-15627

Alignment Scores:
Pred. No.: 1,296-26 Length: 341
Score: 515.00 Matches: 125
Percent Similarity: 50.98% Conservative: 57
Best Local Similarity: 35.01% Mismatches: 115
Query Match: 9.63% Indels: 60
Gaps: 12

US-09-502-945-2 (1-2885) x US-09-902-540-15627 (1-341)
Qy      1481 ACCCAAGTGTGCTACGACACGTTCAATGAAGCACCGTGCATGTGCGGAAACAA 1540
Db      3 SerThrLeuLeuLeuThrAspProLeuPheGlnHisAspProGlyGlnGly----- 20
Qy      1541 CAGTCGACCGTCGATGCTGCGCGATCCAGACGATCTGTGCTCCGCGTCAGAGACA 1600
Db      21 -----HisProGluSerProSerArgLeuArgGlyLeuGlyValLeuAlaSerThr 38
Qy      1601 GGCCTGCTTAGCAAGTCGAGCGGATCCGAGT-----CGCAAGCC 1642
Db      39 -----ProVallyleGlyThrValMetThrAlaProArgSerAla 51
Qy      1643 ACGTTAAGTATCGACGACGATCTGAATACACACACCTGCTGTATGGACCACT 1702
Db      52 ThrGluAlaGluLeuAlaSerValHisThrPro-----GluLeuLeuAlaTyrLeuGln 69
Qy      1703 CCGCTCAAC-----CGGACGAGACTGACAGCAAGAAAGTTGCTGGATCCATCAGCCAG 1756
Db      70 ArgGlyLeuGlnGlyHisArgAlaGlnHisProAspThrGlnValSerPro----- 86
Qy      1757 AAGATGTATGCTGTGCTGCTTGTGGGGGCATCGGGGTGACAGTGAACCGTGTGAAT 1816
Db      86 ----- 86

```

```

Qy      1817 GAGATGCACTCTCCAGTGTGTGCGCATGAGCAGTGGGCTGCTGTGAGACTGGCCTTC 1876
Db      87 -----AspSerValaAspAlaAlaArgLeuAlaAlaGlyAlaSerValGlnAlaValGln 104
Qy      1877 AAGTGGCTGACAGAGAGCTCAAGATGATTTGGCTATCTCGGCCCCAGACACCAAC 1936
Db      105 AlalaMetLeuGlyGlnAlaAlaGlnGlyPheAlaLeuValArgProProGlyHisHis 124
Qy      1937 GCGGAGAAATCCACAGCCATGGATTTGCTTTTCAACTCTGATGAGCAATCAGCCGAAA 1996
Db      125 AlaGluProAspArgValaMetGlyPheCyLeuTyrHisAsnAlaAlaTleAlaAlaGln 144
Qy      1997 CTCCTACAGCAGAAAGTTGAACGTGGGCAAGTCTCTCATCTGATGAGCAATTCACCAT 2056
Db      145 -----AlaGlyArgGlyLeuGlyAlaGluArgValLeuValLeuAspThrAspValHisHis 163
Qy      2057 GGCATGGAACCCAGCAGAGCGTTCTCAATGACCCCTGTGCTTACATCTGTGCAT 2116
Db      164 GlyAsnGlyThrGlnAlaAlaPheThrSerArgArgAspValMetTyrGlnSerValHis 183
Qy      2117 CGCTATGACAAAGGAATCTTTCCAGCTCTGGGGCTCTTGAAGAGTTGTGAGAGA 2176
Db      184 GlnPhePro-----TyrPheProGlyThrGlyAlaAlaProGluValGlyValGly 200
Qy      2177 CCAAGCGTGGGATCAATGTGAACGTGACATGACACAGAGAGTGTGACCCCATTTGA 2236
Db      201 AlaGlyGluGlyTyrThrHisAsnValGlyLeuProGlyGly-----AsnSer 216
Qy      2237 GACGTGAGTACCTTACAGCCTTCAGACAGTGTGATGCCATTTGCCACGAGTTCTCA 2296
Db      217 AspAlaAspTyrGlyMetLeuPheGlnGluLeuLeuLeuProValAlaTyrArg 236
Qy      2297 CCGATGTGCTCTAGTCTCCGCGGTTGATGCTGTGAAGACATCTGTCTCTCTG 2356
Db      237 ProGlnLeuThrLeuValSerAlaGlyPheAspSerHisGln-----His---AspProIle 254
Qy      2357 GGTGGCTACTCTGTGACCGGCAGATGTTTGGCCACTTGACCAAGCAGCTGATGACCTTG 2416
Db      255 GlyGlyMetAspValSerGluArgGlyPheAlaAlaMetCySerAlaMetCySerLeu 274
Qy      2417 GCAAGG-----GGCCGGGTGCTGCGCCCTGAGGAGGCGCATGACTTGAAC 2464
Db      275 AlaAspSerValCysGlnGlyArgLeuValLeuLeuLeuGluGlyTyrSerLeuGln 294
Qy      2465 GCCATCTGTATGCTCTGAAGCTTGTGTCTCGGCTTGTCTCAAGTGAAG 2515
Db      295 GlyLeuSerGlnSerValHisAlaCyValGluValLeuAlaGlyArgGly 311

RESULT 13
US-09-248-796A-15279
; Sequence 15279, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15279
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15279

Alignment Scores:
Pred. No.: 4,426-24 Length: 386

```





QY	2194	TGTAAGCTGGCAATGACACAGAGAGGTGGACACCCCGCATTTGGAGACCGTGAGTACCTTAC	2253
Db	478	MLEuAsnValPro-----LeuIleuProGlyGlyIynHsAraAlaIlyrMetG	494
QY	2254	AGCCTTACAGACACGTGTGATGCCCATTTGCCACGAGTTCTCACCCTGATGTGTGCTTAGT	2313
Db	494	nAlaMetGlnArgIleValIleuProAlaIleuGlnArgPheArgProGlnIleuIleValVa	514
QY	2314	CTCCGCGGGGCTTTGATGTCTTTGAAGACATCTGTCTCTTGGGTGGCTACTCTGTAC	2373
Db	514	ILaISerClyPheAspAla-----AsnAlaValAspProIleuAlaArgMetGlnLeuNI	532
QY	2374	CGCAGATGTTTGTTCACACTTGACAGACAGACTGATGACCCCTG-----GCAGG	2421
Db	532	sSerAspSerPheArgAlaMetClnAlaMetIleArgAspAlaIalagIuaGlnHsAlaIagI	552
QY	2422	GGCGCGGGTGTGTGCTGGCGCTTGAGAGGAGGACCATGACTTGACCGGCATCTGTGATGCTTC	2481
Db	552	YglYArgLeuValValHIsGlnGlyGlyTyr-----Se	564
QY	2482	TGAAGCTTGTGTC-----TGGCTTCTGCTAG	2508
Db	564	rGlnAlaIyTValP:opheCysGlyLeuAlaValIleGlnIleuSerserGlyValArgSe	584
QY	2509	TGTAAGCTGACGCGCTTGATGAGGAGCGCTTGACAGAAAGGCCAAC	2557
Db	584	rAlaValAlaArgAspProIleuArGAspPheIleGlnIleuGlnIleuProIleu	600

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 12, 2005, 00:25:19 ; Search time 30.8712 Seconds

(without alignments)  
6277.336 Million cell updates/sec

Title: US-09-502-945-3

Perfect score: 2140  
Sequence: 1 ggctcgtcgaatcagctcgcga.....gaagaagaagaagaagaaaa 1298

## Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

-MODE=frame+n2p.model -DEV=x1p  
-Q=/cgn2\_1/USPTO.spool\_p/US09502945/runat\_10032005\_164737\_13306/app\_query.faeta.1.10979  
-DB=Issued Patents AA -QPMT=faetan -SUFPRX=mar9.ra1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonsum62 -TRANS=human40.cdl  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09502945 -QCGN\_1.1.283 -@runat\_10032005\_164737\_13306 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -MSG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued Patents AA.\*  
1: /cgn2\_6/prodata/1/1aa/5A COMB .pep.\*  
2: /cgn2\_6/prodata/1/1aa/5B COMB .pep.\*  
3: /cgn2\_6/prodata/1/1aa/6A COMB .pep.\*  
4: /cgn2\_6/prodata/1/1aa/6B COMB .pep.\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS COMB .pep.\*  
6: /cgn2\_6/prodata/1/1aa/backfile1 .pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	401	18.7	434	1	US-08-097-830E-3 Sequence 3, Appl1
2	401	18.7	434	2	US-08-456-112B-3 Sequence 3, Appl1
3	368	17.2	608	4	US-09-270-767-32937 Sequence 32937, A
4	368	17.2	608	4	US-09-270-767-48154 Sequence 48154, A
5	365.5	17.1	235	4	US-09-270-767-36681 Sequence 36681, A
6	365.5	17.1	235	4	US-09-270-767-51898 Sequence 51898, A
7	341.5	16.0	283	4	US-09-270-767-39894 Sequence 39894, A
8	341.5	16.0	283	4	US-09-270-767-55111 Sequence 55111, A
9	326	15.2	71	4	US-09-513-999C-6221 Sequence 6221, Ap
10	313	14.6	611	4	US-09-216-393B-81 Sequence 81, Appl
11	298	13.9	1898	1	US-08-056-200-94 Sequence 94, Appl
12	298	13.9	1898	2	US-08-800-644-94 Sequence 94, Appl

13	298	13.9	1898	4	US-09-538-092-1280 Sequence 1280, Ap
14	291	13.6	411	4	US-09-270-767-41978 Sequence 41978, A
15	281	13.1	745	4	US-10-164-595-80 Sequence 80, Appl
16	281	13.1	784	4	US-10-164-595-79 Sequence 79, Appl
17	281	13.1	843	4	US-10-164-595-54 Sequence 54, Appl
18	272	12.7	919	4	US-09-949-016-65954 Sequence 6594, Ap
19	269	12.6	1240	4	US-09-538-092-658 Sequence 658, App
20	265	12.4	100	2	US-08-460-890A-62 Sequence 62, Appl
21	265	12.4	100	3	US-08-167-641C-62 Sequence 62, Appl
22	265	12.4	100	3	US-08-460-971A-62 Sequence 62, Appl
23	265	12.4	100	3	US-08-462-040-62 Sequence 62, Appl
24	264	12.3	178	4	US-09-489-039A-8236 Sequence 8236, Ap
25	261	12.2	1507	3	US-08-929-329-5 Sequence 5, Appl1
26	256.5	12.0	779	4	US-10-164-595-56 Sequence 56, Appl
27	256.5	12.0	1388	4	US-09-949-016-10817 Sequence 10817, A
28	253.5	11.8	1382	4	US-09-171-991-9 Sequence 9, Appl1
29	252	11.8	309	4	US-09-270-767-46030 Sequence 46030, A
30	247.5	11.6	500	4	US-09-949-016-7692 Sequence 7692, Ap
31	247.5	11.6	712	4	US-09-949-016-10600 Sequence 10600, A
32	246	11.5	793	4	US-09-538-092-1271 Sequence 1271, Ap
33	243	11.4	176	4	US-09-270-767-61576 Sequence 61576, A
34	243	11.4	226	4	US-09-270-767-41210 Sequence 41210, A
35	243	11.4	236	4	US-09-270-767-56426 Sequence 56426, A
36	242.5	11.3	1402	4	US-09-248-796A-14503 Sequence 14503, A
37	240.5	11.2	182	4	US-09-489-039A-8301 Sequence 8301, Ap
38	240	11.2	170	4	US-09-248-796A-27838 Sequence 27838, A
39	239.5	11.2	1564	4	US-10-144-198-4 Sequence 2, Appl1
40	239.5	11.2	1564	4	US-10-144-198-4 Sequence 2, Appl1
41	239	11.2	212	4	US-09-252-991A-19925 Sequence 19925, A
42	239	11.2	1020	4	US-09-538-092-911 Sequence 911, App
43	238.5	11.1	447	4	US-09-171-991-4 Sequence 4, Appl1
44	235.5	11.0	171	4	US-09-489-039A-8235 Sequence 8235, Ap
45	234.5	11.0	432	2	US-08-933-750C-47 Sequence 47, Appl

## ALIGNMENTS

RESULT 1  
US-08-097-830E-3  
; Sequence 3, Application US/08097830E  
; Patent No. 5652211  
; GENERAL INFORMATION:  
; APPLICANT: Porro, Massimo  
; TITLE OF INVENTION: Peptides For Neutralizing The  
; TITLE OF INVENTION: Toxicity of Lipid A  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Hedman, Gibson & Costigan, P.C.  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: diskette, 3.50 inch, 1.44 Mb storage  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/097,830E  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Costigan, James V.  
; REGISTRATION NUMBER: 25,669  
; REFERENCE/DOCKET NUMBER: 576-003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 302-8989  
; TELEFAX: (212) 302-8998  
; INFORMATION FOR SEQ ID NO: 3:



[illegible][illegible]



```
Db      447  sgluglugluarlgylaelugluarlgarlglyslvglugluarlgarlguglugly 467
Qy      1037  GGAAGAAC-----AGAAAAAGTMAAGAAAGAAAGAAAGAAAGAAAGAA 1090
Db      467  sargargluglugluarlgarlglyslvglugluarlgarlglyslvglugluar 487
Qy      1091  AGAAGAACTAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1150
Db      487  garglugluglugluarlgarlglyslvglugluarlgarlglyslvglugluar 507
Qy      1151  AACGAAGAAAGAAATPAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1210
Db      507  ggluglugluarlgarlglyslvglugluarlgarlglyslvglugluar 527
Qy      1211  A-----GAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1246
Db      527  ylyslarlglyslvglugluarlgarlglyslvglugluarlgarlglyslvgl 547
Qy      1247  GCGGAAGAAAGAAAGAAAGTATPAGAAAGAAAGAAAGAAAGAAAG 1296
Db      547  sgluglu-gluarlgarlglyslvglugluarlgarlglyslvglugluar 563
```

```
RESULT 5
US-09-270-767-36681
; Sequence 36681, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 1599-03-17
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 36681
; LENGTH: 235
; TYPE: PR
; ORGANISM: Drosophila melanogaster
US-09-270-767-36681
```

```
Alignment Scores:
Pred. No.: 6,92e-28 Length: 235
Score: 365.50 Matches: 89
Percent Similarity: 58.53% Conservative: 38
Best Local Similarity: 41.01% Mismatches: 62
Query Match: 17.08% Indels: 28
DB: 4 Gaps: 5
```

US-09-502-945-3 (1-1298) x US-09-270-767-36681 (1-235)

```
Qy      659  AGAAGAGGCAAGATGCGACGACGAGCTTCAGAGGCTCGAGTCTACTA 718
Db      7  lyarlglyslvglugluarlgarlglyslvglugluarlgarlglyslvgl 26
Qy      719  TGAAGCAAGCTCGAAGAGAAAGAAATCNAAGTTAAAGTATCAGAACTGTGA 778
Db      27  ArgGlySerGlyVallyslvgllyslvgllyslvgllyslvgllyslvgl 44
Qy      779  GAAAGAAAGCCCAAGAAAGCCCTAAAGAGTTGACAGCTCGGAGGTTAATCCAG 838
Db      45  glygluarglyslvglugluarlglyslvglugluarlglyslvgl 55
Qy      839  TGCCGACTAGAAAGCA-----AGAAAAAGAAAGAAAGAAAGAAAGAA 889
Db      56  ---ArgThrlyslvgllyslvgllyslvgllyslvgllyslvgllyslvgl 74
Qy      890  GAAAGCAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 949
Db      74  ylyslvglugluarlglyslvgllyslvgllyslvgllyslvgllyslvgl 86
Qy      950  AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1009
Db      950  AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1009
```

```
Db      87  -lyslvglugluarlgarlglyslvglugluarlgarlglyslvglugluar 106
Qy      1010  TAAGAAAGAGAGAGAAAGAAATPAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1069
Db      106  uylslvgllyslvgllyslvgllyslvgllyslvgllyslvgllyslvgl 126
Qy      1070  AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1129
Db      126  uylslvgllyslvgllyslvgllyslvgllyslvgllyslvgllyslvgl 142
Qy      1130  GAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1189
Db      142  uylslvgllyslvgllyslvgllyslvgllyslvgllyslvgllyslvgl 162
Qy      1190  GAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1249
Db      162  slslslslslslslslslslslslslslslslslslslslslslslslsl 182
Qy      1250  GAAAGAAAGAAAGAAAGTATPAGAAAGAAAGAAAGAAAGAAAGAAAG 1298
Db      182  glyslvgllyslvgllyslvgllyslvgllyslvgllyslvgllyslvgl 198
```

```
RESULT 6
US-09-270-767-51898
; Sequence 51898, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 1599-03-17
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 51898
; LENGTH: 235
; TYPE: PR
; ORGANISM: Drosophila melanogaster
US-09-270-767-51898
```

```
Alignment Scores:
Pred. No.: 6,92e-28 Length: 235
Score: 365.50 Matches: 89
Percent Similarity: 58.53% Conservative: 38
Best Local Similarity: 41.01% Mismatches: 62
Query Match: 17.08% Indels: 28
DB: 4 Gaps: 5
```

US-09-502-945-3 (1-1298) x US-09-270-767-51898 (1-235)

```
Qy      659  AGAAGAGGCAAGATGCGACGACGAGCTTCAGAGGCTCGAGTCTACTA 718
Db      7  lyarlglyslvglugluarlgarlglyslvglugluarlgarlglyslvgl 26
Qy      719  TGAAGCAAGCTCGAAGAGAAAGAAATCNAAGTTAAAGTATCAGAACTGTGA 778
Db      27  ArgGlySerGlyVallyslvgllyslvgllyslvgllyslvgllyslvgl 44
Qy      779  GAAAGAAAGCCCAAGAAAGCCCTAAAGAGTTGACAGCTCGGAGGTTAATCCAG 838
Db      45  glygluarglyslvglugluarlglyslvglugluarlglyslvgl 55
Qy      839  TGCCGACTAGAAAGCA-----AGAAAAAGAAAGAAAGAAAGAAAGAA 889
Db      56  ---ArgThrlyslvgllyslvgllyslvgllyslvgllyslvgllyslvgl 74
Qy      890  GAAAGCAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 949
Db      74  ylyslvglugluarlglyslvgllyslvgllyslvgllyslvgllyslvgl 86
Qy      950  AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1009
Db      87  -lyslvglugluarlgarlglyslvglugluarlgarlglyslvglugluar 106
```

Dd	108	UGLUGLUYBSGLUYArGAcgLYsgLUGLUglULyBle**LySlyBLySLyGLUAr	128
Qy	1117	-----ACGAAGAAGAAAGAAATAATTAAGAACNAAGAAAGAAAGAAAGAAAG	1163
Dd	128	G**ArgLYglULySLyBSGLUGlu--LySlyBSlyBSGLUGLyBLyArGLyBLyBSlyBS	147
Qy	1164	AATAAGAGAGAGAAAGAAAGAAAGAAAGAA-----	1193
Dd	148	ArgLYBSGLUArgLYBSGLULyBSlyBSGLUwngLUArGLyBLyArGLUGLUArGLyBLyBS	167
Qy	1194	-----ACGAAGAGAAAGAAAGCAAGAAAAGAAAGAAAGAAAGAAAGAAAGT	1241
Dd	168	LySlyBSGLYArGLyBLyArGLyBLyBSlYglULUArGAcgLYsgLUGLUglULyBSlyBSGLU	187
Qy	1242	AGAAACCGAAGAAAGAAAGAAAGCTATTAAAGAGCAGACAGACAGAAAGAAAGAAAA	1298
Dd	188	ArgLUArGLyBSArGcGLUGLUglULyS-----LySGlYLySLyBLySLyGclYglULyBS	204
 RESULT 8 US-09-270-767-55111 ; Sequence 55111, Application US/09270767 ; Patent No. 6703491 ; GENERAL INFORMATION: ; APPLICANT: Homburger et al. ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster ; FILE REFERENCE: File Reference: 7326-094 ; CURRENT APPLICATION NUMBER: US/09/270..767 ; CURRENT FILING DATE: 1999-03-17 ; NUMBER OF SEQ ID NOS: 62517 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 55111 ; LENGTH: 283 ; TYPE: PRT ; ORGANISM: Drosophila melanogaster ; FEATURE: ; OTHER INFORMATION: Xaa means any amino acid  US-09-270-767-55111			
 Alignment Scores:			
Pred. No.:	1.82e-25	Length:	283
Score:	341..50	Matches:	82
Percent Similarity:	66.17%	Conservative:	51
Best Local Similarity:	40.80%	Mismatches:	36
Query Match:	15.96%	Indels:	32
DB:	4	Gaps:	6
 US-09-502-945-3 (1-1298) x US-09-270-767-55111 (1-283)			
Qy	780	AAAGAAAGGCCAAGAAAGCCCTTAAGACTTTTAGCACGCCTCGGAGAGGTTAATCCAGCT	839
Dd	10	LYsglYLySLyBSGLULyBSGLYArGLyBLyBSGLUGLUglULyBLyBSGLYArGLyBLyBS	29
Qy	840	GCCGCACTAAGAAAGCAAGAAAGAGAGAAAGAGAGAGCAGACAGAAAG-----AAG	890
Dd	30	GLULyBSArGLYglULyBLyBSGLULyBSlyBSGLUArgLYBSArGLyBSGLUGLUglULyBS	49
Qy	891	AAAGCAAGCAGAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA	950
Dd	50	LYslYSLyBS***ArgLYBLyBSGLUGLUglULyBSlyBSrg-GLUGLUyBLyBSArGLyBSArG	69
Qy	951	AAGGAGAGAGAGAAAGAAAGAAAGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAA-----	1002
Dd	69	gARGLYLySLyBSlyBSGLYBSGLYUArGLYBSGLUArGLyBSlyBSGLYBSGLYArGLI	89
Qy	1003	-GAAGAActAAGAGAGAGAGAGAGAAATAAGAAAGAGAAAGAGAGAGAGAGAGAGAGAGTNNAA	1061
Dd	89	ULySLyBSGLUArGLYglULyGLUGLUglULyBLyBSGLYArGLyBSArGLYULyBSArGLyS--GI	108
Qy	1062	GAAGAAAG-	1116
Dd	108	UGLUGLUyBSGLUGLyArGArGLyBSGLUGLUglULyBle**LySlyBLySLyBSGLUAr	128
Qy	1117	-----ACGAAGAAGAAAGAAATAATTAAGAACNAAGAAAGAAAGAAAGAAAG	1163

```

Db      128 g***ArgGlyGluIuylsYsGluIu- -LysYsYsGluGluYsArgYsArgYs 147
Oy      1164 AATAAGAGAGGAAAGAAAGAAAGAGAA----- 1193
Db      148 ArgYsGluArgYsGluYsArgYsGluYsGluYsArgYsArgYsArgYsArgYs 167
Oy      1194 -----AAGAGAGGAAAGAGGAAAGAAAGAAAGAAAGAAAGAAAGT 1241
Db      168 LysYsGluYsArgYsGluYsArgYsGluYsGluYsArgYsGluYsArgYs 187
Oy      1242 AGAAAGCGAAGAAAGAAAGAAAGTAAAGAGGAAAGAGAGGAAAGAAAGAA 1298
Db      188 ArgGluArgYsArgYsArgYsGluYs-----LysGluYsYsYsGluYsGluYs 204

RESULT 9
US-09-513-999C-6221
; Sequence 6221, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6221
; LENGTH: 71
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-513-999C-6221

Alignment Scores:
Pred. No.:          3,77e-24          Length:          71
Score:              326.00             Matches:          68
Percent Similarity: 95.77%             Conservative:     3
Best Local Similarity: 95.77%           Mismatches:      0
Query Match:        15.23%             Indels:           0
DB:                  4                  Gaps:            0

US-09-502-945-3 (1-1298) x US-09-513-999C-6221 (1-71)

Oy      11  ATGACTGGGAACCGGCTTGAGAGAGCTTCTGAGCCANCAAGAAAGTAAAG 70
Db      1  MetThrAlaSerGluAlaGluSerLeuAlaLeuSerGluGluGluLeuAla 20
Oy      71  GATTGGCAAAAGACTACTCTTGAGTGAGAGTGAAGATGAGGCGGCAATGATGAGAG 130
Db      21  AspLeuProLysAspYrLeuLeuSerGluSerGluAspGluGluAspAspGlyGlu 40
Oy      131  AGAAAGCATCAAAACCTCTTGAGAGCAATCACTTCCCTTGATGAAAGCATAGCGGAAA 190
Db      41  ArgYsHisGluYsLeuLeuGluAlaLeuSerSerLeuAspGlyYsAsnArgYs 60
Oy      191  TTGCGTGANAGCTCTGAGGCTAGTCTGAAGGTG 223
Db      61  LeuAlaGluArgSerGluAlaSerLeuYsVal 71

RESULT 10
US-09-216-393B-81
; Sequence 81, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDI PROTEINS, NUCLEIC ACID MOLECULES, AND USES THERE
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B

```

[illegible]







Db 456 yshieglungluhrgargluglnargleuhsyargluglnugluhrgarg 474

RESULT 14

US-09-270-767-41978

Sequence 41978, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 41978

LENGTH: 411

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-270-767-41978

Alignment Scores:

Pred. No.:	2, 22e-20	Length:	411
Score:	291.00	Matches:	108
Percent Similarity:	44.728	Conservative:	74
Best Local Similarity:	26.548	Mismatches:	178
Query Match:	13.608	Indels:	47
DB:	4	Gaps:	11

US-09-502-945-3 (1-1298) x US-(9-270-767-41978 (1-411))

QY 92 TTGAGTGAAGTGAAGTGAAGGGAACAATGATGAGAGAGAAAGCATCAAAAGCTTCTTG 151

Db 16 LeuThrllyMeSerSerapSpgluHh1sYrGluprolySalh1sYlsYleu 35

QY 152 GAAGCAATCAAGTCCCTTGATGAGAAAGATAGCGGAATGGCTGAGAGGCT 211

Db 36 Glnh1a1le1a1SerleuGlyValGlnh1s1leGlnh1sSerThrxrYapSpGluArg 55

QY 212 AGTCTGAAGGTGCAGAGTTC-----AATGTCAGTTCTGAAGA 250

Db 56 GlnSerleuGlnAspGlnPheGlnLeuValLySgLYValSerSer1aGlnThraPph1s 75

QY 251 TCAGAGAAAAGCTGGTCTTCGAGATCTGCTTGAGCCTGTTAAAATTATCTTCTTTG 310

Db 76 AlaProxAlaValGlyLeuAsnAspLeuValAsp1leuukrghThSerThrlYsh1s 95

QY 311 GCCACTGTGAAAAAGCACTGAGTAGATC--AAATCAAGAAAGACAGTGGAGTTAAGT 367

Db 96 SerGlnThrlYlsYlsYleuYsaen1le1eGlySer1sYlsYValLeuGlnYspPro 115

QY 368 CTGAACAAAGAAAGAGATGAACGAGATCCACAGAAATAGCATTCATTAATAACGACAAAGT 427

Db 116 LeuGlnLySerProAlaA:aaSPArg-----1leYsaArgInr-11 128

QY 428 C-----CTCTCAATATGGAGCCCTGTGCTCTGAAGAACCG 463

Db 128 eGlyTrYrGlnGlyValThrlYlsYleuGlyArgTTPaSPAlaValVala1aGlnGlnh1a 148

QY 464 GCAGGAGAGAGAGCTGTTTTCCTCGAGAAAGAGAGACCGACCATTCCTCCATTTGA 523

Db 148 gSer1aGlnThrlYlsYleuYsaen1le1ePheProleuYProSerGlnThrlYValYsaThra1a 168

QY 524 ACATGTGCTCAGT---GCGTGAAGGCAAGACATCCCTCGAGCAGAGAAATTT-----572

Db 168 aaenAlaArgProleuYsaenThraYValYlsYsaen1le1eGlnGlnGlnGlnGlnGln 188

QY 573 -----TTCAACCTCTCTCATAGAAAGAGAGACCGACCATTCCTTTA-----617

Db 188 naenArgLySleuAlaYrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 208

QY 618 -CTGACCCCTGTGAAAAGGCTCTCTC---CGAGCCATAGAGCTTGAAGAGGCAAGAT 673

Db 208 ulenAlaYrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 228

QY 674 GCGACGAGAGAGCTTCAGAGGGCTCGGCTCTGCAATCTTAATGANGCCAGGCTCG 733

Db 228 aArgArgLySglnuAlaYrLeuLyMeArGlnuSerGlnYsSer1aYsa1aAr 248

QY 734 AAGAGAGAAAGAAATCAAAAGTTAAAGTATCAACAAGCTCGAGAAAGAGAGCCAA 793

Db 248 gMetGlnh1sYlsYlsYleuYsaen1le1ePheThrlYlsYleuGlnYsaGlnh1sMe1e 268

QY 794 GAAGCCCTTAAAGATTGAGCAGCTCGGAGAGGTTAATCCAGCTGCC-----842

Db 268 uGlnGlnMetLySglnPheGlnLeuGlnh1sYrThraPProGlnAla1leuGlnY 288

QY 843 -----GCATTAAGAAAGAGAGAAAGAGAGAAAGAGAGAGAGAGAGAGAGAG 895

Db 288 sleuSn1a1eGlnGlnYsSerArgValGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 308

QY 896 CAAAGAGAAAGAAAG 955

Db 308 rGlyThrlYrAlaYsaen1le1eArgAlaYsYrYsaPlysaPValArgLySa 328

QY 956 AGAAG 1015

Db 328 pleuAlaGlnGlnLeuAlaValSerArg-----GlnLeuThrlYlsYleu 343

QY 1016 GAAG 1069

Db 343 eGlnGlnSer1aSerSerGlnuAspGlnThrlYlsYsaYrValLeuProGlnGlnGln 363

QY 1070 AAG 1129

Db 363 paSnAPryrAsPProPheAsnProTrThrlYsaYrGlySa1aThrGlnGlnThrlY 383

QY 1130 GAAGATTAAG 1189

Db 383 nGlysaenGlyGlnSerAspGlySerAsnTrpArgGlnYrTrpThrlYsaYrAsnLySe 403

QY 1190 GAAAG 1208

Db 403 rGlnYlsYleuGlnGlnGln 409

RESULT 15

US-10-164-595-80

Sequence 80, Application US/10164595

Patent No. 6657054

GENERAL INFORMATION:

APPLICANT: Origene Technologies, Inc

TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides

FILE REFERENCE: IU 103 RI

CURRENT APPLICATION NUMBER: US/10/164,595

CURRENT FILING DATE: 2002-06-10

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patent In version 3.1

SEQ ID NO 80

LENGTH: 735

TYPE: PRT

ORGANISM: Homo sapiens

US-10-164-595-80

Alignment Scores:

Pred. No.:	2, 73e-19	Length:	735
Score:	281.00	Matches:	98
Percent Similarity:	43.528	Conservative:	80
Best Local Similarity:	23.964	Mismatches:	133
Query Match:	13.138	Indels:	98
DB:	4	Gaps:	13

US-09-502-945-3 (1-1298) x US-10-164-595-80 (1-735)

QY 245 GAAGATCAAGAGAAAGCTGTC-----CTTGCAATCTGCTGAGCCTGTTAAA 295

Db 12 GlnGlyAlaSerGlyYlsYleuGlnAlaPheGlyPheCyGlnYrYrGlnuProGlnuSer 31









```

Db      1589 SerGlnSerLeuMetValProGlnSerGlySerProGluProGluSerIleArgAsnThr 1608
Qy      62 GGTGCGACACGACGAGCTGACCTGGCCACGACCTGACCGAAGAGCCCGAGAAAT 121
Db      1609 SerArgSerSerThrProAlaIlePheAla-Ser---AspProAlaThrCysProIle11 1627
Qy      122 TCCGGCATNAGGTGATTTTCGATTGAAATGATGC----- 158
Db      1627 eProGly-----CysGluThrThrIleGluIleSerly 1638
Qy      159 ----AGAGAGGACTATCTCTATGATGTGCTG----- 186
Db      1638 sglYArgThrGlyLeuGlyLeu-SerIleValGlyIleGlySerAspThrLeuLeuGlyAla1 1658
Qy      187 -----CGAATGTACACACAG-----ACCATGACGCGCGCGCTCGTGG 226
Db      1658 IeIleIleIleHngluValIlyrGluGluGlyAlaAlaCysIlySerGlyArgLeuTrpAlaG 1678
Qy      227 GAGACCTGAACCTGCTCATCAAT----- 249
Db      1678 IyAspGlnIleLeuGluValAAsnGlyIleAspLeuArgIyAlaThrIleAspGluAla1 1698
Qy      250 -----GAACCCAGCCGCTGCTGCTGTTGATGCCATTGCGCCGCTGA 292
Db      1698 IeAsnValIleuArgIlnThrProGlnArgValArgLeu---ThrLeuYrArgAspGlu1 1717
Qy      293 TCCCACTGACAGACACAGGTGAATATGATCAGCTGACGCGCCGCGCGCTCCAGAGAGCTGA 352
Db      1717 IabProYrIlySerGluGluGluValCysAspThrLeuThr----- 1729
Qy      353 AGGAGGTGCGCTTGAACCGCTGACCCCGAAGGCGCTCGGCTGAGTGCTGCTGCGC 412
Db      1730 ----IleGluLeuGlnIlySerProGlyIlySerGlyLeuGlyLeuSerIleValGlyIySa 1748
Qy      413 TGGAGTTTGGCTTGGGCTTTTATCTCCACCTCATCAAAAGCGGTCAAGGACAGACG 472
Db      1748 rGAsn---AspThrGlyValPheValSerAspIleValIySgIyIleAlaAspAla1 1767
Qy      473 TCGGG---CTCCAGTAGAGGAGACAGATGCTCCGGAATGATGATTCATCCCTCC 529
Db      1767 sPglYrIySerMetGlnGlyAspGlnIleLeuMetValAsnGlyGluAspValArgAsn1 1787
Qy      530 GTAACCATGAGAGAGTATCATCAACCTCATTCGA---ACCAAGAAAGCTGTGTCATCAAG 586
Db      1787 IeThrGlnGluAlaValAlaIleLeuLeuLeuLeuLeuLeuLeuGlyThrValThrLeuGly 1807
Qy      587 TGAACAATCGGCTGATCCCGTGAAGAGCTCTCTGATGACCCCTCATTTGGCAGT 646
Db      1807 aI-----GlyArgIleIyAlaGlySerSerThrSerGluSerLeu----- 1820
Qy      647 ATGTGATCATGTTTGTGTGGGATCTGGGGCGTGGAGGACACCTGGGCTCC-----C 700
Db      1821 -----GlnSerSerSerlySerlySerlySerlySerlySerlySerlySerly 1834
Qy      701 CTGGAATCGGGAAGAACAGAGAGAGAGAGAGTCTTTCATCAGCTGATAGCTCCCGAGGCC 760
Db      1834 InglyLeuArgThrValGluMetIlySer-----GlyProThrAspSerI 1849
Qy      761 TTGGCTGACGACATTTCCAGCGGC-----CCCATCCAGAAAGCTGGCATTTTATCA 811
Db      1849 eudIlyIleSerIleAlaGlyIyValGlySerProLeuGlyAspValProIlePheIle1 1869
Qy      812 GCCATGGAACCTGCTCCCTGCTGCTGATGAGTG---GGATTGGAGATAGGGAGACAG 868
Db      1869 IeMetMetCysProThrGlyValAlaAlaGlnThrGlnIlyLeuArgValGlyAspArg1 1889
Qy      869 TTGTGCAAGTCAATGAGCTGACCTTCTTCACTGATCATCAAGAGAGGCTGTAAATGTGC 928
Db      1889 IeValThrIleCysGlyThrSerThrGlnIlyMetThrIleThrGlnAlaValAsnLeu 1909
Qy      929 TGAATAATAGCCGAGCTGACCATCTCATTTAGCTGACGTGGCGGAGACTGTTC 988

```

```

Db      1909 eulYAsnAla---SerGlySerIleGluMetGlnValAlaIleGlyIyAspVal----- 1926
Qy      989 TGACAGACCGGAGCGGCTGACAGAGCGGCGAGCTGAGCTGACCGGACGAGACTTC 1048
Db      1927 -----SerValIleThrGlyIleGlnGlnIleThrProIleAspSerSerLeu1 1942
Qy      1049 TCATGCAAGAGCGGCTGGCGATGAGAGTCCAAACAAGTCTCCAGAGACAGCAGAGATGG 1108
Db      1942 eRPh-----ThrGlyLeuThrSerSerSerIlePheGln----- 1953
Qy      1109 AGCGGCAAGAGAAAGAAATTTGCCAGAGGACAGAGCAAGAGAAATGAGATACCGA 1168
Db      1953 ----- 1953
Qy      1169 AGGAGATGGAACAGATTGTAGAGAGAGAGAGAGAGATTTAAGACAAATGGAAGAGACT 1228
Db      1954 -----AspAsp 1956
Qy      1229 GGGGCTCAAGAGAACAGTACTTGTGCTTAAACATCACTGCTGAGTACACCCAGTAC 1288
Db      1956 eugIyProProGln-----CysIySerIleThrLeuGlnIyArgIyPro----- 1970
Qy      1289 CCTTGGCAAGCCAAAGTATGATCAGAGAGTGAACCTGAGCTGACCGCGAGATGACC 1348
Db      1970 ----- 1970
Qy      1349 TGGATGAGGACAGCAGAGAGAGAGAGAGAGATTTCCGAAATATGAGAGAGCTTTG 1408
Db      1971 --AspIly----- 1972
Qy      1409 ACCCTTACTTATGTTTCAACCCAGAGACAGATCATGSGGAGAGATGTCGGCTCTACGA 1468
Db      1972 ----- 1972
Qy      1469 TCAAGAGAGAGAGATCCTTGAACCTGAGCGGCGGTGAGTCCATTTGG- 1527
Db      1973 -----LeuGlyPheSerIleValGlyIyIyGlySerProIleGly1 1987
Qy      1528 ----AAGTGTGCTTGTCTGCTGTGTATGACGGGAGCTGAGCGGAGTGTGGA 1582
Db      1987 sPleuProIleYrVallysrThrValPheAlaIySerIleAlaIleSerGluAspGlyArg1 2007
Qy      1583 TTGTGAAGGGGACGAGATCATGCAATCAACGCGAAGATTGTGACAGACTACACCTGG 1642
Db      2007 eulYsArgIyAspGlnIleIleAlaValAsnGlyIleSerLeuGlnIyValThrIleG 2027
Qy      1643 CTGAGGCTGACGCTGCCCTGCAGAGAG 1668
Db      2027 IugIlnAlaValAlaIleLeuIyArg 2035

```

## RESULT 2

```

US-09-306-998-3
; Sequence 3, Application US/09306998
; Patent No. 6291173
; GENERAL INFORMATION:
; APPLICANT: Bartel, Paul L.
; APPLICANT: Tavtligian, Sean V.
; TITLE OF INVENTION: MMSC2- An MMAC1 Interacting Protein
; FILE REFERENCE: MMSC2
; CURRENT APPLICATION NUMBER: US/09/306,998
; EARLIER FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 60/084,740
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2037
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-306-998-3

```

```

Alignment Scores: 2.18e-13 Length: 2037
Pred. No.:

```





[illegible][illegible]



```

FILE REFERENCE: MMSCL Gene
CURRENT APPLICATION NUMBER: US/09/233,086
CURRENT FILING DATE: 1999-01-19
EARLIER APPLICATION NUMBER: US 60/071,861
EARLIER FILING DATE: 1998-01-20
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1881
TYPE: PRT
ORGANISM: Homo sapiens
US-09-233-086-3

Alignment Scores:
Pred. No.: 9,77e-13 Length: 1881
Score: 259.50 Matches: 149
Percent Similarity: 37.03% Conservative: 115
Best Local Similarity: 20.90% Mismatches: 232
Query Match: 6.30% Indels: 217
DB: 3 Gaps: 31

US-09-502-945-4 (1-2236) x US-09-233-086-3 (1-1881)
QY 85 CCTGGCCCGAGCCGTGACCGGAAAGTGGCCCGGAAATTCGGGCAATAGGTGATTTCTG 144
DB 169 ProGlySerValAlaAspArgAsp-----GlnArgLeu 179
QY 145 ATTGAATATGATCAGAGAAGACATATCTATGATGTGTCGAATGTACACAGACC 204
DB 180 LysGluAsp-----GlnIleuAlaIleuAsnIleuPro 192
QY 205 ATGAGC-----GTGGCCGTGCTC-----GTGGAGAC 221
DB 193 LeuAspGlnAsnIleuSerHisGlnGlnAlaIleuIleuGlnIleuThrGlySer 212
QY 232 CTGAAGCTGTATC---AATGAACC-----AGCCCTGCTCTG 270
DB 213 LeuArgLeuIleuValAlaArgGluProValHisThrLysSerSerThrSerSerLeu 232
QY 271 TTGTATGCATTTGGCGCTGATCCCATGAAACACAGGTGAAATATGATCAGTGACC 330
DB 233 AsnAspThrThrLeuProGluThrValCysTrpGlyHisValGluGluValGluLeuIle 252
QY 331 CCCCAGCGCTCCAGAAAGTGAAGAGGTGCTGTGACCCGTGACCCCGAAGGCTTC 390
DB 253 AsnAspGlySer-----GlyLeu 258
QY 391 GCGCTAGTGTGGCGTGGCTGTGAGTTGGCTGTGCTCTTCATCTCCACCTCATC 450
DB 259 GlyPheGlyIleValGlyGlyLysThr-----SerGlyValValValArgThrIleVal 276
QY 451 AAAGGCGGTGAGGAGCAGAGCTGGG---CTCCAGGTAGGGAGCAGAGCATCGTCCGATC 507
DB 277 ProGlyGlyLeuAlaAspArgAspGlyArgLeuGlnThrGlyAspHisIleLeuLysIle 256
QY 508 AATGATATTCATCTCTCTCTGTACCCATGAGAGGTCACTCACTCATTCGAAACC--- 564
DB 297 GlyGlyThrAsnValIleGlnGlyMetThrSerGluGlnValAlaGlnIleValLeuArgAsnCys 316
QY 565 AAGAAACTGTGTCTCAATCAAGTGAACACATCGGCTGATCCCGTGAAAACCTCTCT 624
DB 317 GlyAsnSerValArgMetLeuValAlaArgAspProAlaGlyAspIleSerValIleThrPro 336
QY 625 GATGACCCCTCACTTGGCAGTATGTGATCAGTTTGTGCGGAATCTGGGGCGTGGCA 684
DB 337 ProAlaProAlaAlaIleuProValAlaIleuProThrValAlaSerLysGly----- 353
QY 685 GGCAGCCTGGGCTCCCTGGAATTCGGGAAACACAGAGAAGAGGTCTTCATCAGCCTG 744
DB 354 -----ProGlySerAspSerSerLeuPheGluThrTrpAsnAlaGluLeu 368
QY 745 GTR-----GGTCCGAGGCTTGGCTGGCAGACATTTCCAGGCGC 783
DB 745 GTR-----GGTCCGAGGCTTGGCTGGCAGACATTTCCAGGCGC 783

```

```

DB 369 ValArgLysAspGlyGlnSerLeuGlyIleValGlyIleValGlyValAlaGlyThrSerHis 388
QY 784 CCCATCCAGAAAGCTGGCATTTTATCCACCATGTGAACCTGGCTCCCTGTCTGTG 843
DB 389 ThrGlyGluAlaSerGlyIleTrpValLysSerValIleProGlySerAlaIleArgHis 408
QY 844 GTGGGA---TTGAGATAGAGGACCATTTGTGAAAGTCAATGGCTCCACTTCTAAC 900
DB 409 AsnGlyHisIleGlnValAsnAspLysIleValAlaValAspGlyValAsnIleGlnGly 428
QY 901 CTGATCACAAGAGGCTGTAATGTCTGAAATAATGCGGACGCTGACCATCTCCATT 960
DB 429 PheAlaAsnHisAspValValGluValLeuArgAsn----- 440
QY 961 GTAGCTGACCTGGCCGAGGAGCTGTCATGACA----- 993
DB 441 -----AlaGlyGlnValValHisLeuThrLeuValArgLysThrSerSer 457
QY 994 -----GACCGGAGCGGCTGGCAGAGCGCGGACGCTGAG 1029
DB 458 ThrSerProLeuGluProProSerAspArgGlyThrValValGlu-----Pro 473
QY 1030 CTGACGCGGACGAGCTTCTCATGCAAGACGCGCTGCGATGGATCAACAGATCTTC 1089
DB 474 LeuLysProProAlaLeuPheLeuThrGlyAlaValGluThrGluThrAsn---ValAsp 492
QY 1090 CAGAGACACAGCAGATGAGCGGCAAGAGAAAGAAATTCGCCAGAAAGCAGCAGAG 1149
DB 493 GlyGluAspGluGlu-----LysGluArgIleAspThrLeuLysAsn 507
QY 1150 GAAATGAGAGATACCCGAAAGAGATGAACACAGATTGTAGAGAG---GAAAGAAAGTTT 1206
DB 508 AspAsnIleGlnAlaLeuGlnLysLeuGlnLysValProAspSerProGluAsnGluLeu 527
QY 1207 AAGAACCAATGGGAAGAAGATCGGGCTCAAGGAAGACATCTCTGCTTAAACCATC 1266
DB 528 LysSerArgTrpGluAsnLeuLeuGlyProAspTrpGlyValMetValAlaThrLeuAsp 547
QY 1267 ACTGCTAGAGTACACCCAGTACCCCTTCGAAAGCCAAATGATGATCAG----- 1314
DB 548 ThrGlnIleAlaAspAspAlaGluLeuGln-----LysTyrSerLysLeuLeuProIle 565
QY 1315 -----GAGTGAACCTGAG----- 1329
DB 566 HisThrLeuArgLeuGlyValGluValAspSerPheAspGlyHisIleTyrIleSerSer 585
QY 1330 -----CTGAGCCCGCAGATGACCTG--- 1350
DB 586 IleValSerGlyGlyProValAspThrLeuGlyLeuLeuGlnProGluAspGluLeu 605
QY 1351 -----GATGGA----- 1356
DB 606 GluValAsnGlyMetGlnLeuTyrGlyLysSerArgGluAlaValSerPheLeuLys 625
QY 1356 ----- 1356
DB 626 GluValProProProPheThrLeuValCysCysArgArgLeuPheAspGluAlaSer 645
QY 1357 -----GGCAGGAGGAGCAGGAGAGCAG 1380
DB 646 ValAspGluProArgArgThrGluThrSerLeuProGluThrGluValAspHisAsnMet 665
QY 1381 GATTTCCGAAATATGAGAGAGGCTTTGACCCCTCATGTATGTTCACCCGAGACGATC 1440
DB 666 AspValAsnThrGluGluAspAspArgGlyGluLeuAlaLeuThrSerProGlu----- 683
QY 1441 ATGGGAGAGATGTCGGGCTCTTACGATCAAGAGAGAG-----GGATCTTA 1488
DB 684 -----ValLysIleValGluLeuValLysCysLysGlyLeuGlyPheSer 699
QY 1489 GACCTGCGCTGAGAGCGGTGTGACCTCCCATTTGGAAAGTGTGCTTGTGCTG 1548
DB 700 IleLeuAspTrpGlnAspProLeuAspProThrArgSerValIleValIleArgSerLeu 719

```

QY 1549 TATGACGGGAGCTCTGAGCGCATGTGCATTGTGAAGGAGGACGATCATGCA 1608  
DB 720 ValAlaAspGlyValAlaGluArgSerGlyGlyLeuLeuProGlyAspArgLeuValSer 739  
QY 1609 ATCAACGGCAGATTGTGACAGACTACACCTTGAGGCTGACGCTGCTGACAG 1668  
DB 740 ValAlaGluGlyCysLeuAspAsnThrSerLeuAlaGluAla--ValGluLeuLeu 758  
QY 1669 GCGTGAATACAGCGGAGCATGATGACCTTGTG--CTTCCGCTTCCCTCCCA-- 1722  
DB 759 AlaValProProGly-----LeuValHisLeuGlyLeuGlyCysValProLeu 773  
QY 1723 ---AAGAGATGACGATGATGATGACCTTGTGCTG-----AAG 1758  
DB 774 ValGluAspAsnGluGluGluSerCysTyrIleLeuHisSerSerSerAsnGluAsp 793  
QY 1759 TCCAAAGGGGAAACCAATTCAACGCTTGAAGAAACAGT 1797  
DB 794 ThrGluPheSerGlyThrIleHisAspIleAsnSerSer 806  
RESULT 6  
US-09-562-737-21  
Sequence 21, Application US/09562737  
Patent No. 6428967  
GENERAL INFORMATION:  
APPLICANT: Herz, Joachim  
APPLICANT: Gotthardt, Michael  
TITLE OF INVENTION: LDL Receptor Signaling Pathways  
FILE REFERENCE: UTSW0708  
CURRENT APPLICATION NUMBER: US/09/562,737  
CURRENT FILING DATE: 2000-05-01  
NUMBER OF SEQ ID NOS: 132  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 21  
LENGTH: 724  
TYPE: PRF  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-562-737-21  
Alignment Scores:  
Pred. No.: 7 09e-13 Length: 724  
Score: 258.50 Matches: 127  
Percent Similarity: 39.74% Conservative: 90  
Best Local Similarity: 23.26% Mismatches: 200  
Query Match: 6.27% Indels: 129  
DB: 4 Gaps: 25  
US-09-502-945-4 (1-2236) x US-09-562-737-21 (1-724)

QY 610 GTGAAAAGCTCTCTGATGAGCCCTCACTTG--CAGTATGATGATGATGCTG 666  
DB 254 SerTyrAlaProProAspIleThrThrSerTyrSerGlnHisLeuAspAsnGluLeuSer 273  
QY 667 GAATCTGGGGGGCTGCAAGGACCTGGGC-- 696  
DB 274 HisSer-----SerTyrLeuGlyThrAspTyrProThrAlaMetThrProThr 289  
QY 697 -----TCCCTGGAATTCGGAA-----AACAG 720  
DB 290 SerProArgArgTyrSerProValAlaValAspLeuLeuGlyGluAspIleProArg 309  
QY 721 GAGAAAGAGCTTTCATCAAGCTGTGATGAGCTCCGAGGCTTGAGCTGACATTTCCAGC 780  
DB 310 GluProArgArgIleValIleHisArgGlySerThrGlyLeuGlyPheAsnIleValGly 329  
QY 781 GGGCCCATCAAGAGCCTGGCATTTTATGACCATGTC-----AACTGGCTCC 831  
DB 330 GlyGlu--AspGlyGluGlyIlePheIleSerPheIleLeuAlaGlyGlyProAlaAsp 348  
QY 832 CTGCTGCTGAGTGGATGATGAGATAGGGGACAGATGCTGCAAGCATAGGCTGAC 891  
DB 349 LeuSerGlyGlu-----LeuArgGlyGlyAspGlnIleLeuSerValAsnGlyValAsp 366  
QY 892 TTCTTAACCTGATCAACAAGAGCTGTAAATGCTGTAATAATGACCCGACCTGACC 951  
DB 367 LeuArgAsnHisSerIleGluGlnAlaAlaIleLeuYasnAla--GlyGlnThr 385  
QY 952 ATTCATTGTAGCTGACAGCTGCGGAGAGCTGTTCAATGACAGACCGGAGCGCTGGCA 1011  
DB 386 ValThrIleIleAlaGln-----TyrLeuProGluGluTyrSerArgPhe 400  
QY 1012 GAGCGCGGAGGCTGAGCTGACGCGGAGGAGGAGCTTCTCATGCAAGAGCGCTG-- 1065  
DB 401 GluAlaGlyIleHisAspLeuArgGluGln-----LeuMetAsnSerSerLeuGlySer 418  
QY 1066 -----GCGATGAGTCCAAC----- 1080  
DB 419 GlyThrAlaSerLeuArgSerAsnProGlyArgGlyPheTyrIleArgAlaLeuPheAsp 438  
QY 1080 ----- 1080  
DB 439 TyrAspIleThrIleValAspCysGlyPheLeuSerGlnAlaLeuSerPheHisPheGlyAsp 458  
QY 1081 -----AAGATCTCCAGAGCAGCAGAGATGAGCGGCAAGGAAAGAAATTGCC 1134  
DB 459 ValLeuHisValIleAspAlaSerAspGluGluTyrTrpGlnAlaArgArgValHisSer 478  
QY 1135 CAGAAAGCAGCAGAGAAATGAGAGATACCGGAAAGAGATGGAAGATTGTGAGAGAG 1194  
DB 479 AspSerGluThrAsp-----AspIleGlyPheIleProSerTyr 491  
QY 1195 GAAGAGAGTTTAAGAGCAATGGAA-----GAAAGCTGGGGCTCA----- 1236  
DB 492 ArgArgValGluArgArgGluTrpSerArgLeuLeuAlaValAspArgTrpGlySerSer 511  
QY 1237 -----AAGAACAGCTACTCTTGCCCTAAAACCTACT--GCTGAGCTA 1278  
DB 512 GlySerGlnGlyArgGluAspSerValLeuSerTyrGluThrValIleGlnMetGluVal 531  
QY 1279 CAC-----CCATACCCCTTCCGAAAGCCAAATATGATGATGAGAGTGGAACTGAG 1329  
DB 532 HisTyrAlaArgProIleIleIleLeuGlyProThrIleAspArgAlaAsnAspArgLeu 551  
QY 1330 CTGAGCCCGCAGATGACCTGATGAGGCAAGGAGAGCAGGAGAGAGAGATTTCCGG 1389  
DB 552 LeuSerGluPheProAspArgPheGlySerCysValProHisThrIleArgProValArg 571  
QY 1390 AATATGAGAAAGCTTTGACCCCTACTATGTTGACCCCAAGAGAGATGAGGAGGAG 1449  
DB 572 GluTyrGluIleAspGlyArgAspTyrHisPheValSerSerArgGlyValSerGluVal 591  
QY 1450 GATGTCCGGCTCTTACGATCAAGAGAGGAGTCTTGAAGCTGGCCCTGAGAGCGGT 1509





```

Db      414 SerSerLeuGlyLysGlyThraAlaSerLeuArgSerAsnProLeuArgGlyPheTyrIle 433
QY      1093 -----GAGCAGCAGAGATGAGAG 1110
Db      434 ArgAlaLeuPheMetLysThrLysThrLysAspCysGlyPheAsnSerGlnAlaLeuSer 453
QY      1111 CGGCAAAAGAGAAACAAATTGCCAGAAAGCAGAGAGAAATAGAGATACCGG--- 1167
Db      454 PheHisPheGlyGlnValLeuHisValIleAspAlaSerAspArgGlyLysTrpGlnAla 473
QY      1168 -----AAGGATGAGACAGATT-----CTAAGACAGAGAAAGAAAG 1203
Db      474 ArgArgValHisThrAspSerGlnThrAspAspIleGlyPheValProSerLysArgArg 493
QY      1204 TTTAAGACCAATG-----GAGAGACATGCG----- 1230
Db      494 ValGluArgArgTrpTrpSerArgLeuLysAlaLysAspTrpTrpLysSerSerGlySer 513
QY      1231 ---GGCTCAAGAGACAGTACTCTTGCCTAAACATCACT---GCTGAGGTACAC--- 1281
Db      514 GlnGlyArgGlnLysAlaSerValLeuSerTyrGlnThrValThrAspMetGlnValHisTyr 533
QY      1282 -----CCAGTACCCCTTGCAGAACCAAGTATGATCAGGAGATGAGACCTGAGCTCGAG 1335
Db      534 AlaArgProIleGlnIleLeuGlyProThrLysAspArgAlaPheAspAspLeuLeuSer 553
QY      1336 CCGCAGATGACCTGATGAGGACGACGAGACGAGACGAGAGAGAGATTTCCGGAATAT 1395
Db      554 GluPheProAspGlyPheGlySerCysValProHisThrThrHisProLysValArgGlyTyr 573
QY      1396 GAG---GAAAGCTTTGACCCCTACTGTATGTTCAACCCAGAGACATCATGGGAAAGAT 1452
Db      574 GluIleAspGlyIleAsp---TyrHisPheValSerSerArgGlnLysMetGlnLysAsp 592
QY      1453 GTCCGGCTCTTACGACATCAAGAAAGAGGATCTTACAGCTGGCCCTGGAAGGC---GGT 1509
Db      593 IleGlnAlaHisLysLeuIleGlnAlaGlyGlnTyrAsnSerHisMetTyrGlyThrSer 612
QY      1510 GTGCACTCCCTCC-----ATTGGAAGAGTGTCTGTT 1539
Db      613 ValGlnSerValArgAsnValAlaGlnGlnGlyLysHisCysValIleGlnAspValSerAla 632
QY      1540 TCTGTCTGTATGAGCAGGAGCTGCTGAGCGGCAT-----GGTGCATTTGAAAGGG 1593
Db      633 AsnAlaValArgArgArgGlnAlaAlaHisLysHisProIleAlaSerPheIleArgPro 652
QY      1594 -----GACGAGATCATGCAATCAACGCAATCTGTGACAGATACACCTGGCCT 1644
Db      653 ArgSerLeuGlnAsnTrpLeuGlnIleAsnLysArgIle-----ThrGlnVal 668
QY      1645 GAGGCTGACGCTGCCCTGAGAGAGCTGGAATCAGAGCGGAGCTGATCGACCTTTG 1704
Db      669 GlnAlaArgLysAlaPheLeuAspArgAlaTrpLysLeuGlnGlnIleuPheTrpGlnCysTyr 688
QY      1705 GTTGCCGCTC 1713
Db      689 SerAlaIle 691

```

```

RESULT 9
US-09-270-767-42903
; Sequence 42903, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 42903
; LENGTH: 533
; TYPE: PRT

```

```

; ORGANISM: Drosophila melanogaster
US-09-270-767-42903
Alignment Scores:
Pred. No.: 9,05e-11 Length: 533
Score: 232.50 Matches: 82
Percent Similarity: 42.15% Conservative: 71
Best Local Similarity: 22.59% Mismatches: 114
Query Match: 5.64% Indels: 96
DB: 4 Gaps: 13
US-09-502-945-4 (1-2236) x US-09-270-767-42903 (1-533)
QY      340 TCCAGAGACGTGAAGAGAGGCTGCTGACCCGTTCGACCCCGAAGGCTTCGCTGAGT 399
Db      190 SerGlyGlnAlaGlnGlnValValLeuProLys---AsnGlnGlySerLeuGlyPheSer 208
QY      400 GTGCGTGTGGCTCGAGCTTGGCTGT-----GGGCTCTTC 435
Db      209 IleIleGlyGlyThrAspHisSerCysValProPheGlyThrArgGluProGlyIlePhe 228
QY      436 ATCTCCACCTATCAAGAGCGGCTCAGAGACAGGCTCGG---CTCCAGTAAAGGAC 492
Db      229 HisSerHisIleValProGlyValIleAlaSerLysCysGlyLysLeuArgMetGlyAsp 248
QY      493 GAGATGCTCCGATCATGATGATATTCATCTCTCTCTGATCCATGAGAG---GTCAATC 549
Db      249 ArgIleLeuLysValAlaAsnGlnLysValSerLysValAlaThrHisGlnAspAlaValLeu 268
QY      550 AACCTCATTCGAACCAAGAAACCTGTCTCATCAAGTACAGACATCGGCTGATCCCC 609
Db      269 GluLeuLeuLysProGlyAspGlnIleLysLeuThrIleGlnHis----- 283
QY      610 GTGAAGAGCTTCCTGATAGCCCTCATCTTGACAGTATGAGATCAGTTGTGTGCGAA 669
Db      284 -----AspProLeuProProGlyPheGlnGlnValLeuLeuSerLys 297
QY      670 TCT-----GGGCGCTGCGAGGACCTGGGCTCC 699
Db      298 AlaGlnGlyLysArgLeuLysMetHisIleLysGlyLysAlaGlnGlyLysAla 317
QY      700 CCTGGAATCGGGAACCAAGAGAAAGAGCTTTCATACGCTGTAGGCTCCGAGGC 759
Db      318 ProAlaAspProSerAspGln----- 324
QY      760 CTTGCTGACGATTTCCAGCGGCCCATCCAGAAAGCTGACATCTTATCAGCCATGTG 819
Db      325 -----GlyAlaPheValSerLysIle 331
QY      820 AAACCT---GGTCCCTGTCTGTAGGTGAGATTGAGATAGGAGACAGATTTGCA 876
Db      332 AsnSerValGlyAlaAlaArgArgAspGlyArgLeuLysValGlyMetArgLeuGln 351
QY      877 GTCAATGCGCTGACCTTCTTAACCTGATCAACAGAGAGCTTAAATGTCTGAAAAAT 936
Db      352 ValAsnGlyHisSerLeuLeuGlyAlaSerHisGlnAspAlaValAsnValLeuAspAsn 371
QY      937 AGCCGACGCTGACCATCTCATTTGATGAGCTGAGCGGAGGCTGTTCATGACAGAC 996
Db      372 -----AlaGlyAsnGlnIleGlnLeuVal---Va 380
QY      997 CGGAGCGGCTGACAGAGCGGCGGACGCTGAGCTGACAGCGGAGAGCTTTCATGACAG 1056
Db      380 LysLysGlyTyrAspLysSerAsnLeuLeuHisSerIleGlyGlnAlaGlyLysMetSer 400
QY      1057 AAGCGCTGCGCATGAGTCCACAAGATCC-----TTCAGAGACAGACAGATGAGAG 1110
Db      400 rTrpGlyPheAsnSerSerLysSerCysSerGlyLysSerArgGlnGlySerArgLysIle 420
QY      1111 CGGCAAAAGAGAAAGAAATTCGCCAGAGGACGA-----GAGGAA 1152
Db      420 rGluThrGly--SerLysLeuSerGlnSerGlnSerValSerSerLeuAspHisGlnGln 439

```

```
QY 1153 AATGAGATACCGAGAGATGAAACAGATTGTAGAGAGAGAGATTAAAG 1212
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 440 AaPgluAhrGleuAhrGlnAaPheAaPValPheAlaSerGln-----LysPro 455
QY 1213 CAATGGAGAGACATGGGGCTCAAG----- 1239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 456 AaPAlaGlnGlnProThrGlyProSerValLeuAlaAlaAlaAlaMetValHisGly 475
QY 1240 GAACAGCTACTGTGGCTAAACATCATCTGAGTACACCCAGTACCCCTCGCAG 1299
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 476 AlaSerProThrProProAlaAlaAlaThrSerAsnLleThrProLeuProThrAlaAla 495
QY 1300 CCA 1302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 496 Pro 496

RESULT 10
US-09-562-737-23
/ Sequence 23, Application US/09562737
/ Patent No. 6428967
/ GENERAL INFORMATION:
/ APPLICANT: Herz, Joachim
/ APPLICANT: Gotthardt, Michael
/ TITLE OF INVENTION: LDL Receptor Signaling Pathways
/ FILE REFERENCE: UTSW0708
/ CURRENT APPLICATION NUMBER: US/09/562,737
/ NUMBER OF SEQ ID NOS: 132
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 23
/ LENGTH: 724
/ TYPE: PR1
/ ORGANISM: Artificial Sequence
/ FEATURE: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Sequence
US-09-562-737-23

Alignment Scores:
Pred. No.: 2,31e-10 Length: 724
Score: 228.50 Matches: 123
Percent Similarity: 39.01% Conservative: 97
Best Local Similarity: 21.81% Mismatches: 207
Query Match: 5.55% Indels: 137
                Gaps: 26

US-09-502-945-4 (1-2236) x US-09-562-737-23 (1-724)
QY 340 TCCAGAGAGCTGAAGAGAGTGGCTGTGACCGTCTGACCCGAGAGCTCGGCTGAGT 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 155 AlAGluLysAlaLleLleGlnLysTyrLleLys---GlyProLysGlyLeuGlyPheAla 173
QY 400 GTGCGTGGTGGCTG-----GAGTTTGCTGTGG-----CTTTCATCTCCAC 444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 174 LleAlaGlyLysAlaGlyAaGlnLleAaPProGlyAaPAsnSerLleTyrValThrGlu 193
QY 445 CTGATCAAGAGCGCTGAGGAGACAGCGTGGG---CTCCAGTAGGAGGAGAGATGTC 501
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 194 LleLleGlnGlyLysAlaAlaAlaLysAaPheGlyAaGlnLleLleGlyAaPValLleGly 213
QY 502 CGGATCAATGATATTCATCTCTCTCTGTAACCATAGAGAG---GTTCATCAACCTCAT 558
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 214 AlaValAaPAsnSerValGlyLeuGlnAaPheAlaMetHisGlnAaPValAlaAlaLleLle 233
QY 559 CGAAGCAAGAAACCTGTGTCATCAAGTAGA-----CACATCGGCTGATCCCGTG 612
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 234 AaThrThrAaPValValTyrLeuLysLysAlaLysAaPAsnAlaTyrLysSerLeu 253
QY 613 AAAAGCTTCCTGATGAGCCCTCAGCTGG-----CAGTATGATGATCAGTTTGTCG 666
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 254 SerTyrAlaProProPheLleThrThrMetTyrSerGlnHisLeuAaPAsnGlnLleAaP 273
QY 667 GAATCTGGGGGCTGCGAGGAGCAGCTGGG----- 696
```

```
Db 274 HisSer-----SerTyrLeuGlyThrAspTyrGlnThrAlaMetThrProThr 289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 697 -----TCCCTGGAATCGGAA-----AACAG 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 290 SerProArgSerTyrSerProValAlaLysAaPLeuLeuThrGlnLysPheProArg 309
QY 721 GAGAGAGAGCTTTCATCAGCCCTGATAGCTCCCGAGGCTTGCTGACATTTCCAGC 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 310 GluProArgValLleValLleHisArgGlySerThrGlyTyrPheLysAsnLleValGly 329
QY 781 GGGCCCATCCAGAGCGCTGGCATTTTATCAGCATGTG-----AACTGGCTCC 831
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 330 GlyGlu---AspTyrGlnGlyLlePheLleSerPheLleLeuAaPValProAlaAaP 348
QY 832 CTGCTGCTGAGGTGGATTTGAGATAGGGAGACCAATGTGTCAATGCAATGGCGTCAGC 891
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 349 LeuSerGlyGlnLysLysLysAaPAsnLleLeuSerValPheGlyValAaP 366
QY 892 TTCTTAACCTGATCACAAGAGAGCTGTAAATGTGCTGAAATAGCCGACCTGACC 951
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 367 LeuArgAaPAlaSerHisGlyGlnAlaAlaLleAlaLeuLysAaPAlaHisGln---Thr 385
QY 952 ATCTCATTTGATGCTGACGCTGGCGGAGCTGTTCATGACACACCGGAGCGCTGGCA 1011
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 386 ValThrLleLleAlaGln-----TyrLleProGlnLysTyrSerArgPhe 400
QY 1012 GAGCGCGGAGCGGTAGCTGACGCGGAGAGCTTCTCATGCAAGAGCGGCTGGATG 1071
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 401 GluAlaLleLleHisAaPLeuArgGlnLleMetMetSerLeuGlySerGlyThr 420
QY 1072 GAGTCCAAAGATCTCTCCAGAGCAGACAGAGATGAGCGGCAAGAGAAAGAAATT 1131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 AlaSerAaPArg-----SerAaPProLysAaGlyPhe 431
QY 1132 GCCCAGAGGCGACAGAGAAATGAGAGATCCGAGAG----- 1170
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 432 TyrGlnArgAlaLeuPheAaPThrAaPValSerArgAaPValLysPheLeuSerGlnAla 451
QY 1170 ----- 1170
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 452 LeuThrPheHisPheGlyAaPValLeuHisValAlaAaPAlaSerAaPValThrProThr 471
QY 1171 GAGATGGAACAGATTTGATGAGAGAGAAAGATT----- 1206
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 472 GlnThrArgArgValHisSerAaPAsnSerGlnThrTyrAaPValLleGlyPheLleProSerLys 491
QY 1207 -----AAGAGCAATGGGAA-----GAGACCTGGGCTCA 1236
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 492 ArgAlaValAlaGlnArgArgGlnThrPheSerArgLeuAaPAlaLysAaPValThrGlySerSerSer 511
QY 1237 -----AAGAAACAGTACTCTTGCTTAAACCTCACT---GCTGAGGTA 1278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 512 GlyGlnGlnGlyArgGlnAaPAsnSerValLeuSerPheGlnThrValThrGlnMetGlnVal 531
QY 1279 CAC-----CCAGTACCCCTTGCAGGCCAAAGTATGATGAGGAGAGTGAACCTGAG 1329
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 532 HisGlyAlaArgProLleLleLleGlnGlyProHisLysAaPArgAlaAaPAsnAaPLeu 551
QY 1330 CTGAGCCCGGAGATGATGCTGATGAGGAGCAGGAGAGCAGAGAGAGAGATTTCCGG 1389
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 552 LeuLleGlnPheProAaPValPheGlySerGlyValProHisLleThrThrArgProLysG 571
QY 1390 AAATATGAGAGAGCTTTGACCCCTTCTATGTTTACCCGAGAGCATCATGGGAGAG 1449
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 572 GluLeuGlnLysAaPValArgAaPValHisPheMetSerSerArgLysMetGlnLys 591
QY 1450 GATGTCGGCTCTAGCATCAAGAGAGGAGTCTTGAACCTGAGCCCTGGAAGCGGT 1509
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 592 AaPAsnGlnAlaHisLysAaPValLleGlnAlaGlyArgTyrAaPAsnHisLysTyrThr 611
QY 1510 GTGAGCTCCCAATTTGGAGAGTGTCT-----GTTTCT 1542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db	612	SerterginserValArxigluValAlaIleuglnThrIyShiSeYsIleuAspValser	631
Qy	1543	GCTGTGATGAGCGGGAGCTCTGACGGCATGGTGGCATTTG-----	1587
Db	632	AlaValAlaValArxigluIleuAlaIleThrGhiProIleAlaIlePheIleArg	651
Qy	1588	-----AAAGGAGAGATATATGGCATTCACGGCAAGATTGTGACAGACTACACCTG	1644
Db	652	ProTySerIeuGluAsnValIleuGluIleAsnAlaArgIleThrGluIleuAlaArg	671
Qy	1642	GCTAGAGCTACGGCTGC-----CTGCAGAAAGCGCTCAATTCAG-----	1680
Db	672	LysAspPheAspArgAlaThrIyLeuIleuGlnIlePheThrGluCyPheSerAlaIle	691
Qy	1681	---GGCGGGGAGC 1689	
Db	692	ValGlyGlyAsp 695	
RESULT 11			
US-09-562-737-26			
; Sequence 26, Application US/03562737			
; Patent No. 6428967			
; GENERAL INFORMATION:			
; APPLICANT: Herz, Joachim			
; TITLE OF INVENTION: LDL Receptor Signaling Pathways			
; FILE REFERENCE: UTSW0708			
; CURRENT APPLICATION NUMBER: US/09/562,737			
; CURRENT FILING DATE: 2000-05-01			
; NUMBER OF SEQ ID NOS: 132			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 26			
; LENGTH: 724			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURES:			
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic			
; OTHER INFORMATION: Sequence			
US-09-562-737-26			
Alignment Scores:			
Pred. No.: 1.08e-09 Length: 724			
Score: 220.50 Matches: 126			
Percent Similarity: 38.05% Conservative: 81			
Best Local Similarity: 23.16% Mismatches: 218			
Query Match: 5.35% Indels: 119			
Db: 4 Gaps: 24			
US-09-502-945-4 (1-2236) x US-09-562-737-26 (1-724)			
Qy	346	AAGCTGAGAGAGTGCCTCTGACCCGCTGACACCCGAGAGCCTCGAGTGAATGGCT	405
Db	157	LysIleIleGluIleIyLeuIleIyS---IyrrPolyGlyIleuGlyPheSerIleuAla	175
Qy	406	GCTGGC-----CTGGAGTTTGGCTGTGGCTTTTCATCTCCACCTCATC	450
Db	176	AlaGlyValAlaGluAsnGlnHisIleProGlyGluAsnSerIleTyValThrIySIIle	195
Qy	451	AAAGCGGCTACGGAGCAGCGTGGGCTC---CAGGTAGGGAGAGATGTCGGAGTC	507
Db	196	PheGlyGlyAlaIleAlaHisIyAspSerIyArgGlyGlnIleGlyAspIySIIleuAlaVal	215
Qy	508	AATGAGATTTCCATCTCCTCTGTACCAT---GAGAGAGTATCATCACTTGTGAACC	564
	::::	::::	::::
Db	216	HisSerValIleGlyLeuGluAspValMethIstIleAspAlaValAlaIleuIyAsnThr	235
Qy	565	AAGAAATGTGTCCAAAGTGAAGACATCGGCTGTATCCCGTGAAGACTCT---	621
Db	236	LysAspValValTyLeuIyValAlaIyLeuSerAsnAlaTyLeuSerAspSerTy	255
Qy	622	-----CCTGATGAGCCCTCTACATTGG---CAGTATGTGAGATCAATTGTGTGGAAATCT	672
Db	256	MetProPheAspIleThrIySerTySerAsnHisIleuAspAsnGluIleSerHisSer	275

675 GGGGGCGCTGGAGGACACCTGGCTCC-----CTGGAAATGGGAAACAGAGAGAG 726

276 -----GlnTylLeuGIlyThrAProThrAlaArgThrProThrSerPro 291

727 AAGCTTTTCATCAGCCCTGTA----- 747

292 ArgArgTyrSerSerValAlaIlyAerLeuLeuGIlyGluThrIleProArgGluPro 311

748 -----GCTCCCGAGGCTTGGCTGGACATTTCCAGGGGGCC 786

312 ArgArgIleValIlnAerGlySerThrGIlyLeuGIlyThrIleValGIlyGlu 331

787 ATCCAGAAAGCTGGCATCTTTATGAGCGCATGTGAAACCTGGC-----TCCCTGTCT 837

332 ---AerGIlyGluGIlyTyrPheIleSerPheIleLeuAlaGIlyGluAlaAerLeuSer 350

838 GCTGAGGTGGGATTTGAGATrAGGGGACCAATGTGTCATGCAATGGCGCTGACTTCT 897

351 GlYlyIu-----LeuAArgIlyAerAerGlnIleLeuSerValAerGlyValGIlyLeuArg 368

898 AACCTGGATGACAGAGAGGCTGTAAATGTGTGTAATAATGGCCGACCTGCACATCTCC 957

369 AsnAlaSerThrValGluGlnAlaPheIleAlaLeuIlyAsnAlaI---GIlyGlnThrGIlyThr 387

958 ATTGTGCTGGACCTGGC----- 975

388 IleIleAlaGlnTyrIlyProGlnIleIlyTyrSerArgPheGlnAlaIlyIleIleu 407

976 CGGAGAGCTGTTCATGACAGACCCGGAGACCGCTGGCAAGCGCGGACCCGAGACTCCAG 1035

408 ArgGIlyGlnLeuIleuThrAerSerSerGIlySerGIlyThrAlaSerLeuAerSerLeuPro 427

1036 CGGAGAGAGCTTCTCATGACAGAGACCGGCTGGCGAGTGCACAG----- 1083

428 LysArgGIlyPheTyrIleArgAlaMerPheAerTyrThrIlySerTyrIleAerCysAerPhe 447

1084 -----ATCTCCAGAGACACAG 1101

448 LeuSerGlnAlaLeuSerPheThrValGIlyAerValIleuThrIleAerAlaAerAer 467

1102 GAGATGGAGCGGCAAGAGAGAAAGAAATGGCCCGAAGGACGACAGAGAAATGAGAGA 1161

468 GluGIlyTyrTrpGlnAlaArgAerSerThrIleSerAerSerGIlyThrAerAerIleThrPhe 487

1162 TACCGAAGAGATGAGAAACAGATTGTAGAGAGAGAGAGAAATTAAAGAACAAATGGGAA 1221

488 IleProSerIlyAerAerGluValGIlyValArgGIlyThrPheArgLeuGIlyAlaIlyTyr-- 506

1222 GAAAGCTGGGCTCA-----AAGAAACAGCTAACTTTCCTGAAA 1260

507 -----TrpGIlySerSerSerGIlySerGIlyGluTyrGIlyIlyAerSerValLeuSerTyrGlu 524

1261 AACCATCTACT---GCTGAGTACAC-----CCAGTACCCCTTCCCAAGCCAAATAT 1308

525 ThrIleAlaThrGlnMetGIlyValIlnIleTyrAlaArgAerIleIleIleLeuGIlyProThrIlyA 544

1309 GATCAGGAGAGTGAACCTGACCTGGACCCGACATGACCTGGATGGAGGACGACGAGAG 1368

545 AerGlnIlyAerAerAerLeuLeuSerGIlyThrPheAerAerIlyAerPheGIlySerCysValPro 564

1369 CAGGAGAGAGAGATTTCCGAAATrATGAGAGAGCTTGGACCCCTCATATTTCAACC 1428

565 HisGIlyThrAerProIlyAerGIlyTyrGIlyIleIleValAerAerTyrIlnIlePheValSer 584

1429 CCAGAGACAGATGAGGAGAGAGATGTCCGCTCTGACGATCAAGAGAGAGATCTTTA 1488

585 SerIleGluIlyMetGIlyIlyAerGIlyGlnAlaIlyAerPheIleGlnAlaGIlyGlnTyr 604

1489 GACCTGGCCCTGAAAGC---GCTGTGACTCC----- 1518

605 AsnIleuThrIleuTyrGIlyThrSerValGlnSerThrAerArgIleValAlaGIlyGlnIlyA 624



```
QY 1519 ---CCCATGGGAAGTGGTCTGTTCTGCTGTATGAGCGGGAGCTGCTGAGCGGCAT 1575
Db 625 HieAenIleuAaspValSerAlaAenAlaValGlnArgLeuGlnAlaHisLeuHis 644
QY 1576 GGTGGCATTTGTG-----AAAGGGACGAGATCATGGCAATCAACGGCAAG 1620
Db 645 ProArgAlaIlePheIleArgProArgSerLeuSerAsnValLeuGluIleAsnLysArg 664
QY 1621 ATTGTGACAGATPACACCTGGCTGAGGCTGACGCTGCCCTGCAGAAAGCGCTGGAATCAG 1680
Db 665 IleValGluGluGlnAla-----ArgLysAlaPhe-----674
QY 1681 GCGCGGGAGCTGG 1692
Db 675 -----AspTrp 676

RESULT 12
US-09-919-497-98
; Sequence 98, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 1736
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-98

Alignment Scores:
Pred. No.: 1,736-09 Length: 1736
Score: 220.50 Matches: 135
Percent Similarity: 36.71% Conservative: 108
Best Local Similarity: 20.39% Mismatches: 244
Query Match: 5.35% Indels: 175
DB: 4 Gaps: 28

US-09-502-945-4 (1-2236) x US-09-919-497-98 (1-1736)
QY 358 GTGCGTCTGCAGCGTCTGCACCCGAGCGCTGAGTGTGCTGGCTGGAG 417
Db 12 ValThrLeuHisArgAlaProGlyPheGlyPheGlyIleAlaIleSerGlyGlyArgAsp 31
QY 418 -----TTTGGCTGTGG-----CTTCTCATCTCCACCTCATCAAGCGGT 459
Db 32 AsnProHisPheGlnSerGlyGluThrSerIleValIleSerAspValLeuLysGlyGly 51
QY 460 CAGGCGACAGCGTCCGGCTCAGGTAGGGACGAGATCGTCGGATCAATGATATCC 519
Db 52 ProAlaGluGly---GlnLeuGlnGluAsnAspArgValAlaMetValAsnGlyValSer 70
QY 520 ATCTCTCTCTGATCCCATGAGGAGTGCATCACTCATTCGA---ACCAAGAAACTGTG 576
Db 71 MetAspAsnValGluHisAlaPheAlaValGlnGlnLeuArgLysSerGlyLysAsnAla 90
QY 577 TCATCAAAAGTGAACACATCGGC-----CTGATCCCGCTGAAAAGCTCTCTGATGAG 630
Db 91 LysIleThrIleArgArgLysLysValGlnIleProValSerArgProAspProGlu 110
QY 631 CCCTCAGTGGCAGTATGTGGATCATGTTGTGTGCGAATCTGGGCGCTGCGAGCAGC 690
Db 111 ProValSerAspAsnGluGluAspSerTyrAspGluGluIleHisAspProArgSerGly 130
QY 691 CTGGGCTCCCTCGGAATCGGNAACAAGGAG-----723
Db 131 ArgSerGlyValValAsnArgSerGluLysIleTrpProArgAspArgSerAlaSer 150
```

```
QY 723 -----723
Db 151 ArgGluArgSerLeuSerProArgSerAspArgSerValAlaSerSerGlnProAla 170
QY 724 AAGAAGTCTTTCATCAGCTGCTAGCTCCCA-----GGCCTTGGCTGCAGCAT 774
Db 171 LysProThrLysValThrLeuValLysSerArgLysAsnGluGluTyrGlyLeuArgLeu 190
QY 775 TCAGCGGCGCCATCCAGAAGCTGTCATCTTTATCAGGCATCTGTAACACCTGCTCCCTG 834
Db 191 AlaSer-----HisIlePheValLysGluIleSerGlnAspSerLeu 204
QY 835 TCTGTGAGGTGGGA---TTGGAGATAGGGACCAAGATTGTCGAAGTCAATGCGCTGCAC 891
Db 205 AlaAlaArgAspGlyAsnIleGlnGluGlyAspValValLeuLysIleAsnGlyThrVal 224
QY 892 TTCTCTAACCTCGATCACAAGGAGGCTGTAAATGTCTGCTGAAAAATAGCCGACCTGACC 951
Db 225 ThrGluAsnMetSerLeuThrAspAlaLysThrLeuIleGluArgSerLysGlyLysLeu 244
QY 952 ATCTCTCAATTGTAGCTGCAGCTGCGCGGAGCTGTTTC-----ATGACAGAC 996
Db 245 LysMetValValGlnArgAspGluArgAlaThrLeuLeuAsnValProAspLeuSerAsp 264
QY 997 CCGGAGCGCTGCGACAGCGCGCGAGCGT-----GAGCTGACGCGGAGGAG 1044
Db 265 SerIleHisSerAlaAsnAlaSerGluArgAspAspIleSerGluIleGln-----281
QY 1045 CTTCTCATGCAGAGCGGCTGCGAGTGGAGTCCACACAGATCTCCAGGAGCAGGAGG 1104
Db 282 -----SerLeuAlaSerAspHisSerGlyArgSerHisAspArg 294
QY 1105 ATGGAGCGCAAGAGAGAAAGAAATTGCCAGAGGACGACAGAGAAATAGAGATAC 1164
Db 295 ProProArgArgSerArgSerArgSerProAspGlnArgSerGluProSerAspHisSer 314
QY 1165 CGNAAGGAGATGGAACAG-----ATTGTAGAGGAGGAAGAAGTTT 1206
Db 315 ArgHisSerProGlnGlnProSerAsnGlySerLeuArgSerArgAspGluGluArgIle 334
QY 1207 AAGACCAATGGAGAGAGACTGGGCTCAAAGGAACACTACTCTGCTTAACACATC 1266
Db 335 SerLys-----ProGlyAlaVal 340
QY 1267 ACTGTGTAGGTACACCCAGTACCCCTTCGCAAGCCAAATGATGATCAGGAGTGAACCT 1326
Db 341 SerThrProValLysHisAlaAspHisThrProLysThrValGluGluVal-----358
QY 1327 GAGCTCGAGCCCGCAGATGACCTGGATGGAGCAGCAGGAGCAGGAGCAGGATTC 1386
Db 359 -----ThrValGluArgAsnGluLysGlnThr 367
QY 1387 CGAAATATGAGGAAGGCTTTGACCCCTACTCTATGTGTTCCACCCAGCAGCAG-----1437
Db 368 ProSerLeuProGluProLysProValTyrAlaGlnValGlyAsnGlnMetTrpIleTyr 387
QY 1438 -----ATCATGGGG 1446
Db 388 LeuSerValHisLeuMetValSerTyrLeuIleGlnLeuMetLysMetGlyPheLeuArg 407
QY 1447 AAGGATGTCCGCTCCTACGCATCAAGAAGGAGGATCTCTAGACCTGCCCTGGAGGC 1506
Db 408 ProSerMetLysLeuValLysPheArgLysGlyAspSerValGlyLeuArgLeuAlaGly 427
QY 1507 GGTGTGACTCCCATTCGGAAGGTGTCGCTTTCTGCTGTATGATCAGCGGGAGCTGCT 1566
Db 428 GlyAsnAsp-----ValGly---IlePheValAlaGlyValLeuGluAspSerProAla 444
QY 1567 GAGCGCATGTGTCATTTGTAAGAGGAGCAGATCATCGCAATCAACGCAAGATTGTG 1626
Db 445 AlaLysGlu---GlyLeuGluGluGlyAspGlnIleLeuArgValAsnAsnValAspPhe 463
```



Db 517 GluAspSerValLeuSerTyrTrpThrValThrGlnMetGluValHisTyrTyrArgPro 536  
QY 1285 GTACCCCTTCGCAAGCAAGATATGATCAGGGAGTGGAACTCGAGCTCGAGCCCGCAGAT 1344  
Db 537 IleIleIleLeuGlyProThrAlaAspArgAlaAsnAspLeuLeuSerAspPhePro 556  
QY 1345 GACCTGGATGGAGCAGGAGGAGCAGGAGCAGGATTCGCGAAATATGAGGAAGC 1404  
Db 557 AspLysPheGlySerCysValGluHisThrThrArgProLysArgGluTyrPheIleAsp 576  
QY 1405 TTTCAGCCCTACTCTATGTTCCACCCAGCAGCAGATCATGGGGAAGGATGTCGGCTCCTA 1464  
Db 577 GlyArgAspTyrHisPheValGlySerArgGluLysMetGluLysAspIleHisAlaHis 596  
QY 1465 CGCATCAAGAAGGAGGATCCTTAGACCTGGCCCTGGAAGC 1506  
Db 597 LysPheIleGluAlaGlyGlnIleAsnSerHisLeuTyrGly 610

RESULT 14  
US-09-252-991A-21827  
; Sequence 21827, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 21827  
; LENGTH: 1093  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21827

Alignment Scores:  
Pred. No.: 5,73e-09 Length: 1093  
Score: 213.00 Matches: 212  
Percent Similarity: 33.02% Conservative: 67  
Best Local Similarity: 25.09% Mismatches: 302  
Query Match: 5.29% Indels: 264  
DB: 4 Gaps: 47

US-09-502-945-4 (1-2236) x US-09-252-991A-21827 (1-1093)

QY 2190 AGAGTAAGGTTTGGAGTGAACAATC-----CTGGCAGCAATT 2155  
Db 375 ArgValArgLeuAlaAlaProIleArgArgProProArgLeuSerArgLeuAlaAla 394  
QY 2154 AGAGCAGAGGCGAGA-----GGAGAGGGA 2131  
Db 395 ArgValLysAlaArgSerLeuGluLeuSerProProAlaProLeuSerThrAlaProSer 414  
QY 2130 TGGAGAGAGAGACTCCAGTGGGGTCTATTAT----- 2098  
Db 415 TrpArgSerSerAlaProGlyValAlaIleArgProProSerArgLeuThrSerVal 434  
QY 2097 -----GGGTTCAAGGAAGGAGTCCCGCCCAAGCTGG 2068  
Db 435 ProProLeuArgSerArgValThrProValSerLeuThrArgThrProProArgTTP 454  
QY 2067 GAGAGACCAATTTCATGGGCCAGAGAAAGGAATGAGACTCGGATCTTGAGATCTTC 2008  
Db 455 SerArgProPheArgLeuAlaSerSerArgProLeuAlaLeu----- 468  
QY 2007 TCCCAACGGCTGGCTGC---TCCCTTCTCCACATTCGCTTCAAAAAGTGGCCGA 1951  
Db 469 -----ThArgProCysTrpProLeuSerSerArgAlaAla-ThrArgValMetProAl 486

QY 1950 GCTGTTCTTATCTGCGCCCTGTTTCAGGGCCAAAGGAGATTGTCAGATTCTCTGGGTGAT-- 1893  
Db 486 aLeuLeuProMetProPro-----LeuArgLeuLeuSerSerTh 499  
QY 1892 -----AGATTACAGTCCCAAGGATGTCATCTGGTGTGTGTCATGTGGCTCTCTCAAG 1840  
Db 499 rProValArgIleSerThrAlaProLeuAlaLeuIleThrProGluArgLeuLeuSerAr 519  
QY 1839 GCTGTGTCGAGGCTTTGTGTTTCACGAGTGGGGCCGAGCTCAGTCTTCTTCAACCGTG 1780  
Db 519 gLeuAlaProCysSerVal---ThrProAlaSerLeuSerLeuProPro----- 535  
QY 1779 AATTGGTTTCCCTTTTGGACTTCAGCAAGAGGTTCAGCTCATCTGTCATCTTCTTGG 1720  
Db 536 ---Trp-----LeuSerSerAlaAlaTrpLeuValSe 545  
QY 1719 GGGGCAGACGGCAACCAAGGTTCAGTCCCGCCCTGATTCCAGGCCCTTCTGCAG 1660  
Db 545 rAlaSerAlaProAlaLeuGluLysVal-----ProPro-----ArgLeuSerAr 560  
QY 1659 GGCAGCGTCAGCCTTCAGCCAGGGTGTAGTCTGTGTCACAATCTTGCCGTGTGATGCCATGAT 1600  
Db 560 gArgAlaAlaArgAlaValArgLeuProSerLeuThr----- 572  
QY 1599 CTCGTCCCTTTTCACAATGCCACCATGCGCTCAGCAGCTCCCGCTCATACACAGAGA 1540  
Db 573 -----SerAlaProProTrpLeuSerSerThrProProArgLeuThrLeuAr 588  
QY 1539 AACGACCACCTTCCCAATGGGGAGTCCACACCGCTTCCAGGGCCAGGCTCAAGGATCC 1480  
Db 588 gLeuPheTrpLeu-----SerSerArgProProSerProLeuAsnSerSerProPr 605  
QY 1479 CTCCTTCTTTGATGCGTAGGAGCGGACATCTTCCCATGATCTGCTCTGGGGTGAACAT 1420  
Db 605 oSer-----ArgLeuArgProSerArgPro----- 613  
QY 1419 AGAGTAGGGTCAAGCCTTCTCATATTTCCGGAATCTGCTCT-----CC 1372  
Db 614 -----AlaSerThrProLeuAlaTrpPheSerArgArgCysThrValArgArgPr 631  
QY 1371 CTGCTCC-----TCGTGCTCCATCCAGGTTCATCTGGGGCTCGAGCTCAGGTTCCAC 1318  
Db 631 oLeuSerProMetThrLeuProProArgLeuSerSerCys-SerArgAlaPheThrAlaT 651  
QY 1317 TC-----CCTGATCATATTTGGCTTCGGAAGGGGTACTGGGTG 1279  
Db 651 hrPheGluValLeuGluIleSerProAlaArgLeuSerThrCysArgAlaSerIleAlaM 671  
QY 1278 TACCT-----CAGCAGTGTATGTTTGTAGCAAGAGTAGCTGTCTTCTTGA 1234  
Db 671 etProProPheAlaAlaIleSerGlnAspTrpLeuLeuSerIleVal-----S 687  
QY 1233 GCCCAGCTCTTCTCCCATTTGCTTAAACTCTCTTCTCTCT-----CTAC 1186  
Db 687 erAlaAlaThrPheArgValPheSerLeuThrSerSerProProCysTrpAlaArgLeuP 707  
QY 1185 AATCTGTTCCA-----TCTCTTCCGGTATCTCTCATTTCTCTGCTGCTTCTGGGC 1132  
Db 707 roSerValAlaCysArgSerProLeuAlaAlaIleArgProProAlaLeuProThr---- 725  
QY 1131 AATTTCTTTTCTTTCCTGCTCCATCT-----CCTGCTGCTCTGGAGGATCTGTT 1078  
Db 726 -----AlaPheAlaAlaArgSerArgArgProSerLeuAsnSerLeuProProT 742  
QY 1077 GGACTCCATCGCCAGCGCTTCTGCATGAGAGCTCTCCCGCTGCGAGCTCAGCTGCGCG 1018  
Db 742 rpSerLeuArgLeuAlaThrSerThrArgThrProAla-LeuProLeuAlaLeuPro 761  
QY 1017 -----CGCTCTGCGCAGCGCTCCCGGTCTGTGATGAACAGCTCCCGGCGACGTGAGC 964  
Db 762 ProSerArgLeuSerLysAlaProProValAla-----Leu-LysProAlaSerAl 778

```
QY 963 TACAATGGAGATGGTCAGGCTG---CGGCTATTTTTTCAGCACATTTACAGCCCTCCTTTGTG 907
Db      |||||
QY 778 aThrSerThrProProArgLeuSerArgLeuAlaProTTrpThrPheAsnSer-----795
Db      |||||
QY 906 ATCCAGGTTAGAGAACTCAGCCATTGACTTCGACAATCTGGTCCCTATCTCCATCC 847
Db      |||||
QY 796 -LeuArgLeuAspSerArgProProAlaArgLeuSer-----SerCysPr 810
Db      |||||
QY 846 CACCTCAGCAGCAGGAGCGAGGCTTTCATAGGCTGATAAAGATGCCAGGCTTCTGGAT 787
Db      |||||
QY 810 oThrValThrArgCysAlaPro-----TrpLeuSerArgLeuProSer-----824
Db      |||||
QY 786 GGGCCCGCTGGAATCTCGAGCCAAAGGCT-----CGGAGCCTCACCAGGCT 739
Db      |||||
QY 825 -----SerArgLeuSerSerArgProProArgLeuThrSerArgProProArgLe 841
Db      |||||
QY 738 GATGAAGACTTCTCTCTCTGTTTCCCGATTTCCAGGGAG-----696
Db      |||||
QY 841 uLeuSerValProLeuProLeuLeuSerArgLeuArgAlaArgSerArgArgLeuAl 861
Db      |||||
QY 696 -----696
Db      |||||
QY 861 aAlaGluAsnLysProArgArgLeuSerMetAlaProLeuAlaThrThrSerArgSerSe 881
Db      |||||
QY 695 -----CCAGGCTGCTCGCAGCGCCCGCAGATTCGACACAAACTGATC 652
Db      |||||
QY 881 rProLleSerLeuProProArgLeuSerArgLeuPro-----ThrArgAlaSe 897
Db      |||||
QY 651 CACATCTGCCAAGTGAGGGCTCATCAGGAGAGCTTTTCAGGGGATCAGGCCGATGTG 592
Db      |||||
QY 897 rThrArgLeuProGluThrSerProSerProArgLeuThrSerAla-----TrpAl 914
Db      |||||
QY 591 TCTCACTTTGTGACACAGATTCTTCTGTTGGAATGAGGTTGATGACCTCTCATGGGT 532
Db      |||||
QY 914 aLeuThrArgValAspCysTrpLeuProSerArg-----ProCysTrpPr 929
Db      |||||
QY 531 ACAGGAGGAGATGGAATATCCATTGATCCGAGCATCTGCTCCCTTACCTGGAGCCCGAC 472
Db      |||||
QY 929 oLeuSerSerValAlaAlaProThrSerArgSerPheArgProLleThrTrpProProAr 949
Db      |||||
QY 471 GCTGCTGCTGACCGCCTTTGTG-----AAGAGCCACAGCCAACTCCAGGCC 445
Db      |||||
QY 949 gLeuSerArgSerProArgValLeuThrThrAlaArgSerArgLeuCysAsnArgProSe 969
Db      |||||
QY 444 GTGGGAGATG-----AAGAGCCACAGCCAACTCCAGGCC 409
Db      |||||
QY 969 rTrpArgLeuSerArgLeuLeuAlaSerThrArgSerSerProSerAlaSerSerLeuPr 989
Db      |||||
QY 408 ACCACGCACATCAGGCCGAGGCTTCGGGGTGCAGACGGTCCAGACGCACCTCTTCAG 349
Db      |||||
QY 989 oProArgLeuSerArg-----CysProProSerThrArgThrValAlaPr 1004
Db      |||||
QY 348 CTTCTGGAGCGCGGGGTGACGTGATCATATTCACCTGGTGTTCAGTGGGATCAG 289
Db      |||||
QY 1004 oPheArgLeuProProTrpLeuSer-----SerAlaTrpLeuAlaPheAlaSerSe 1021
Db      |||||
QY 288 CGGCCGAATGGCATCAACAGAGGCAGACGGCTGGGTTTCATTG-----ATGAC 241
Db      |||||
QY 1021 rAlaArgLeuAlaThr-----ArgLeuProAlaLeuArgArgValProLeuArg 1037
Db      |||||
QY 240 CAGCTTCAGGCTCTCCACG-----AGCAGCGCCACGCTCCATGCT 202
Db      |||||
QY 1037 gSerSerArgSerProArgAlaLeuArgArgSerSerGlySerThrProAlaSer-----1055
Db      |||||
QY 201 CTGGTGGTACATTCGACGACATCATAGAGATAGTCTCTCTGTCATCATTTTCAATCAG 142
Db      |||||
QY 1056 -----IleThrProAlaLeuSerArgArgAlaAlaSerSerAlaMetArgSerAr 1072
Db      |||||
QY 141 AAATCCACTTATGCGG---AATTCTCGGCCACTTTTTCGTCATCGCTGGCGCCAGG 85
Db      |||||
QY 1072 gAlaAlaArgLeuCysArgLeuThrSerSerSerAlaLeuArgIleSerAlaLeuPro---1091
Db      |||||
QY 84 TCCAGCT 78
```

```
Db      |||||
QY 1092 -ProAla 1093
Db      |||||
RESULT 15
US-09-949-016-9739
; Sequence 9739, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9739
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9739

Alignment Scores:
Pred. No.: 1,33e-08 Length: 428
Score: 206.00 Matches: 124
Percent Similarity: 37.00% Conservative: 61
Best Local Similarity: 24.80% Mismatches: 184
Query Match: 5.00% Indels: 131
DB: 4 Gaps: 20

US-09-502-945-4 (1-2236) x US-09-949-016-9739 (1-428)
QY 47 GCACCCGAGGAGGAGCGGTCTGCAACG-----ACGCTGAGCCTGCCCGACCA 97
Db      |||||
QY 12 AlaProArgGlySerArgArgProThrValProGlyThrProAlaCysLeuAlaArgPro 31
Db      |||||
QY 98 TGGACCGGAAAGTGGCCCGAGAAATTCGCGCATPAGGTGGATTTCTCTGATTGAAATGATG 157
Db      |||||
QY 32 AlaAlaGlnGlyPheSerAlaAlaLeuProValArg-----43
Db      |||||
QY 158 CAGAGAAGACTATCTCTATGATGTGCTGCGGAATGTATCCACAGACCATGAGCGTGGCG 217
Db      |||||
QY 44 -----TrpThr-GlyAr 47
Db      |||||
QY 218 TGCTCGTGGAGACCTGAAGCTGGTTCATCAATGAACCCAGCCGCTGCTGCTCTGTTGTATG 277
Db      |||||
QY 47 gArgAlaGly-----ProSerArgProValProLl 57
Db      |||||
QY 278 CCATTTCG-----GCCGCTGATCCCACTGAAGCACCACGTGGAATATGATCAGCTGA 328
Db      |||||
QY 57 eGlyThrProSerArgAlaAlaAspProSerGln-----GlyGluMetSerAlaAs 74
Db      |||||
QY 329 CCCCCCGCGCTCCAGGAGCTGAAGAGGTGCGTCTGGACCGTCTGCACCCCGAGGCC 388
Db      |||||
QY 74 pAlaAlaAla-GlyAlaProLeuProArgLeuCysLeuGluLysGlyProAsnGlyT 94
Db      |||||
QY 389 TCGGCTGAGTGTGCTGCTGGCTGGAGTTTGGC---TGTTGGCTCTTCATCTCCAC 445
Db      |||||
QY 94 yGlyPheHisLeuHisGly-----GluLysGlyLysLeuGlyGlnTrpIleArgLeu 112
Db      |||||
QY 446 TCATCAAGAGCGGTTCAGGACAGCAGCGTCCGGCTCCAGGTAGGGACGAGATCGTCCGGA 505
Db      |||||
QY 112 alGluProGlySerProAlaGluLysAlaGlyLeuLeuAlaGlyAspArgLeuValGluV 132
Db      |||||
QY 506 TCATGGATATTCATCTCCTCTTACCATGAGAGGTATCAACCTCATCTTCGAAACCA 565
Db      |||||
QY 132 alaAsnGlyGluAsnValGluLysGluThrHisGlnGlnValValSerArgIleArgAla- 151
Db      |||||
```





GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 12, 2005, 00:25:19 ; Search time 51.4203 Seconds  
(without alignments)  
6277.336 Million cell updates/sec

Title: US-09-502-945-5

Perfect score: 3989

Sequence: 1 cctggccgcgtcgcggtgc.....tattttccagcttaaaaaa 2162

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p,model -DSV=slp  
-Q/cgn2\_1/USPTO\_spool\_p/US09502945/runat 10032005 164737 13306/app query.fasta\_1.10979  
-DB=issued Patents AA -QFMT=fastan -SUFFIX=mar9.rai -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09502945 @CGN 1.1 283 @runat 10032005 164737 13306 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCUTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	273	6.8	2046	4	US-09-949-016-9365
2	263	6.6	2037	4	Sequence 9365, Ap
3	250.5	6.3	1881	3	Sequence 3, Appli
4	234.5	5.9	767	4	Sequence 69, Appli
5	234.5	5.9	767	4	Sequence 59, Appli
6	232.5	5.8	533	4	Sequence 42903, A
7	232	5.8	1771	4	Sequence 9470, Ap
8	229.5	5.8	724	4	Sequence 21, Appli
9	225	5.6	1736	4	Sequence 98, Appli
10	211	5.3	724	4	Sequence 28, Appli
11	210.5	5.3	724	4	Sequence 23, Appli
12	206.5	5.2	1050	3	Sequence 50, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-949-016-9365  
; Sequence 9365, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 9365  
; LENGTH: 2046  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9365

Alignment Scores:  
Pred. No.: 1.05e-14  
Score: 273.00  
Percent Similarity: 36.78%  
Best Local Similarity: 24.75%  
Query Match: 6.84%  
DB: 4  
Length: 2046  
Matches: 146  
Conservative: 71  
Mismatches: 170  
Indels: 203  
Gaps: 25

US-09-502-945-5 (1-2162) x US-09-949-016-9365 (1-2046)

QY 11 TCGCGTCCGCGCTCTTTCCAGCTCTCGCAGCCGCCGCGAA-----GGAAACG 61

Sequence 12, Appli  
Sequence 12, Appli  
Sequence 2, Appli  
Sequence 46, Appli  
Sequence 46, Appli  
Sequence 49, Appli  
Sequence 2, Appli  
Sequence 3, Appli  
Sequence 14, Appli  
Sequence 15, Appli  
Sequence 16, Appli  
Sequence 32, Appli  
Sequence 22, Appli  
Sequence 3, Appli  
Sequence 30, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 9739, Ap  
Sequence 30843, A  
Sequence 33426, A  
Sequence 48643, A  
Sequence 8945, Ap  
Sequence 26, Appli  
Sequence 24, Appli  
Sequence 26065, A  
Sequence 21827, A  
Sequence 29, Appli  
Sequence 13, Appli  
Sequence 16789, A  
Sequence 25101, A  
Sequence 4, Appli

5.1 2466 3 US-09-080-855-12  
5.1 2466 4 US-09-566-076-12  
5.1 2466 5 PCT-US94-09943-2  
5.1 2485 4 US-09-290-640-46  
5.1 2485 4 US-09-665-615B-46  
5.1 1050 3 US-09-045-632-49  
5.1 1112 3 US-09-045-632-2  
5.1 1112 3 US-09-045-632-3  
5.0 604 3 US-09-045-632-14  
5.0 702 3 US-09-045-632-15  
5.0 1018 3 US-09-045-632-16  
5.0 1061 3 US-09-045-632-32  
5.0 724 4 US-09-562-737-22  
5.0 2465 2 US-08-596-291-3  
5.0 2465 3 US-09-100-804-3  
4.9 724 4 US-09-562-737-30  
4.9 450 2 US-08-665-037-2  
4.9 450 2 US-08-666-067-2  
4.9 450 2 US-08-732-870-2  
4.8 428 4 US-09-949-016-9739  
4.9 663 4 US-09-252-991A-30843  
4.8 131 4 US-09-270-767-33426  
4.8 131 4 US-09-270-767-48643  
4.8 534 4 US-09-949-016-8945  
4.8 724 4 US-09-562-737-26  
4.7 724 4 US-09-562-737-24  
4.7 836 4 US-09-252-991A-26065  
4.8 1093 4 US-09-252-991A-21827  
4.7 724 4 US-09-562-737-29  
4.7 507 3 US-09-045-632-13  
4.6 774 4 US-09-252-991A-16789  
4.6 917 4 US-09-252-991A-25101  
4.6 358 4 US-09-740-027-4





```
DB: 3 Gaps: 26
US-09-502-945-5 (1-2162) x US-09-306-998-3 (1-2037)
QY 11 TCAGCGTTCGGCGCTCTTTCCAGCTCTCGGAGCGGGCCAGCCGAA-----GGAACG 61
DB 1552 SerGlnSerLeuMetValProGlnSerGlySerProGluProGluSerIleArgAsnThr 1571
QY 62 GGTGCTGCAACGACGAGCTGGACCTGGCCAGCCATGGACCGAAAGTGGCCCGAGAAAT 121
DB 1572 SerArgSerSerThrProAlaIlePheAla-Ser---AspProAlaThrCysProIleI 1590
QY 122 TCCGGCATAGGTTGGAATTTCTGATTGMAAATATGC----- 158
DB 1590 eProGly-----CysGluThrThrIleGluIleSerLy 1601
QY 159 ----AGAGAAGGACTATCTATGATGTGCTG----- 186
DB 1601 sGlyArgThrGlyLeuGlyLeu-SerIleValGlyGlySerAspThrLeuLeuGlyAlaI 1621
QY 187 -----CGAATGTATCCACCAG-----ACCATGGAGCTGGCGCTCTCGTGG 226
DB 1621 leIleIleHisGluValTyrgluGluGlyAlaAlaCysLysAspGlyArgLeuTipAlaG 1641
QY 227 GAGACCTGAAGCTGCTCATCAAT----- 249
DB 1641 lyAspGlnIleLeuGluValAlaAsnGlyIleAspLeuArgLysAlaThrHisAspGluAlaI 1661
QY 250 -----GAACCCAGCGCTCTGCTCTGCTGTTGATGCCATTCGCGCGCTGA 292
DB 1661 leAsnValLeuArgGlnThrProGlnArgValArgLeu---ThrLeuTyArgAspGluA 1680
QY 293 TCCCACTGAAGCACAGGTGGAATATGATCAGCTGACCCCGCGCGCTCCAGGAAGCTGA 352
DB 1680 laProTyrylsGluGluValCysAspThrLeuThr----- 1692
QY 353 AGAGAGTGGCTTGGACCGTCTGCACCCGAGCGCTCGCGCTGAGTGCTGGTGGCC 412
DB 1693 -----IleGluLeuGlnLysLysProGlyLysGlyLeuGlyLeuSerIleValGlyLysA 1711
QY 413 TGGAGTTTGGCTGTGGCTCTTCATCTCCACCTCATCAAGCGCTCAGGACAGACG 472
DB 1711 rgAsn---AspThrGlyValPheValSerAspIleValLysGlyIleAlaAspAlaA 1730
QY 473 TCGGG---CTCCAGGTAGGGAGAGATCGTCCGGATCAATGATATTCATCTCTCTCT 529
DB 1730 spGlyArgLeuMetGlnGlyAspGlnIleLeuMetValaAsnGlyGluAspValArgAsnA 1750
QY 530 GTACCCATGAGGAGGTATCACTCATTCGA---ACCAAGAAACTGTGTCCATCAAG 586
DB 1750 laThrGlnGluAlaValaAlaLeuLeuLysCysSerLeuGlyThrValThrLeuGluV 1770
QY 587 TGAGACATCGCGCTGATCCCGTGAAGCTCT-----CCTGATGAG----- 630
DB 1770 aIGlyArgIleLysAlaGlyProPheHisSerGluArgProSerGlnSerSerGlnV 1790
QY 631 -----CCCTCACTTGGCAGTATGTGATCACT 658
DB 1790 aISerGluGlySerLeuSerSerPheThrPheProLeuSerGlySerSerThrSerGluS 1810
QY 659 TTGTGTCGGAATTCGGGGCGTCGAGGAGCGCTCGGGCTCC-----CCTGGAATTCGGG 712
DB 1810 erLeu---GluSerSerSerLysAsnAlaLeuAlaSerGluIleGlnGlyLeuArgT 1829
QY 713 AAAACAAGGAGAGAGGTCTTCATCAGCTGTGAGCTCCGAGCGCTTGGTCGAGCA 772
DB 1829 hrValGluMetLysLys-----GlyProThrAspSerLeuGlyIleSerI 1844
QY 773 TTTCACGCGC-----CCCATCCAGAAGCGCTGTCATCTTTATCAGCCATCGAAAC 823
DB 1844 leAlaGlyValGlySerProLeuGlyAspValProIlePheIleAlaMetMetHisP 1864
QY 824 CTGGCTCCCTGTCTGTGAGGTG---GGATTGGAGATAGGGACCAAGATTGTGCAAGTCA 880
```

## RESULT 3

```
US-09-233-086-3
; Sequence 3, Application US/09233086
; Patent No. 6337192
; GENERAL INFORMATION:
; APPLICANT: Bartel, Paul L.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: MMSC1 - An MMAC1 Interacting Protein
; FILE REFERENCE: MMSC1 Gene
; CURRENT APPLICATION NUMBER: US/09/233,086
; CURRENT FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: US 60/071,861
; EARLIER FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1881
```

```
1864 roThrGlyValAlaAlaGlnThrGlnLysLeuArgValGlyAspArgIleValThrIleC 1884
QY 881 ATGCGCTCGACTTCTCTAACCTGATCAAGAGGAGCTGTAAATGTGCTGAAATAAGCC 940
DB 1884 ysGlyThrSerThrGluGlyMetThrHisThrGlnAlaValaAsnLeuLeuLysAsnAla- 1903
QY 941 GGAGCTGACCATCTCCATTTAGCTGAGCTGGCCGGAGCTGTTTCATGACAGACGGG 1000
DB 1904 --SerGlySerIleGluMetGlnValAlaGly-GlyAspValSerValValThrGly 1922
QY 1001 AGCGGCTGCAGAGCGCGCGAGCTGAGCTGCAGCGCGAGGAGCTTCTCATCAGAAC 1060
DB 1922 ----- 1922
QY 1061 GGTGCGCATGGATGTCACAAAGATCTCCAGGAGCAGCAGAGATGCGAGCGGCAAGGA 1120
DB 1922 ----- 1922
QY 1121 GAAAGAAATTCGCCAGAAAGCGCAGAGAGAGAAATGAGAGATACCGGAAGGAGATGGAAC 1180
DB 1922 ----- 1922
QY 1181 AGATTGTAGAGGAGGAGAGAGAGTTTAAAGAGCAATGGGAAGAGACTGCGGCTCAAAG 1240
DB 1922 ----- 1922
QY 1241 AACAGCTACTTTCCTAAACCATCACTGCTGAGGTACACCCAGTACCCCTTTCGCAAGC 1300
DB 1923 -----HisGlnGlnGluProAlaSerSer 1930
QY 1301 CAAAGTGATTCGGAATAATAGGAAGGCTTTGACCCCTACTCTATGTTTACC----- 1354
DB 1931 SerLeuSerPhe-----ThrGlyLeuThrSerSerSerIlePheGlnAspAsp 1946
QY 1355 -----CCAGACGATCATGCGGAGGATGTCGGCTCTCAGCATCAAGAGAGGAGGA 1408
DB 1947 LeuGlyProProGlnCys-----LysSerIleThrLeuGluArg-----GlyProAsp 1962
QY 1409 TCTTAGACTCGCGCTGGAAGCGGTGGAGCTCCCGCATTTGG-----AAGGTGGTC 1462
DB 1963 GlyLeuGlyPheSerIleValGlyGlyTyrglySerProHisGlyAspLeuProIleTy 1982
QY 1463 GTTCTGCTGTATGAGCGGGAGCTGCTGAGCGGATGTTGGCATTTGTGAAAGGGGAC 1522
DB 1983 ValLysThrValPheAlaLysGlyAlaAlaSerGluAspGlyArgLeuLysArgGlyAsp 2002
QY 1523 GAGATCATGGCAATCAACGGCAAGATTGTGACAGACTACACCTGCTGAGCTGAGCTG 1582
DB 2003 GlnIleIleAlaValaAsnGlyGlnSerLeuGluGlyValThrHisGluAlaValAla 2022
QY 1583 GCGCTGCAGAAAG 1594
DB 2023 IleLeuLysArg 2026
```

```

i      TYPE: PRT
;      ORGANISM: Homo sapiens
US-09-233-086-3

Alignment Scores:
Pred. No.:      9,3e-13      Length:      1881
Score:          250.50      Matches:      155
Percent Similarity: 36.03%      Conservative: 117
Best Local Similarity: 20.53%      Mismatches:  281
Query Match:      6.28%      Indels:       202
DB:              3          Gaps:         28

US-09-502-945-5 (1-2162) x US-09-233-086-3 (1-1881)
QY 70  AACGCGCAGCTGGACCTGGCCCGCCAGCCATGGACCGAAAGTGGCCGAGAAATTCGGCAT 129
D 70  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 991  AenAspValGlnGlyProSerLeuLeuIleAspLeuProValAlaGlnArgArgGlu 1010
D 991  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 130  AAGGTGGATTTCTGATTGAAATGATGACAGAGAGGACTATCTCTATGATGTGTGCGA 189
D 130  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1011  GlnGluAsp-----LeuPro 1015
QY 190  ATGTAC---CACAGACCACTGACGCGCGCTGCTGCTGGGAGACTGAAGCTGTGTCATC 246
D 190  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1016  LeuTyrGlnHisGlnAla-----ThrArgValIle 1025
QY 247  AATGAACCCAGCGCTGCTCTGTTTGATGCAATTCGCGCGCTGATCCCACTGAAGCAC 306
D 247  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1026  SerLysAlaSer-----AlaTyrThrGlyMetLeuSerSerArgTyr 1039
QY 307  CAGGTGGAATATATCATCAGCTGACCCCGCGCTCCAGGAAGCTGAAGGAG----- 357
D 307  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1040  AlaThrAspThrCysGlnLeuProGluArgGluGluGlyGluGlyGluGluThrProAsn 1059
QY 358  -----GTGCGTCTGGACCGTCTGCGACCCCGCGCTGCGACCCCGGAGGCGCTC 390
D 358  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1060  PheSerHisTrpGlyProProArgIleValGluIlePheArgGluProAsnValSerLeu 1079
QY 391  GCCTGAGTGGCGGTGGC-----CTGGAGTTTGGC----- 423
D 391  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1080  GlyIleSerIleValGlyGlyGlnThrValIleLysArgLeuLysAsnGlyGluGluLeu 1099
QY 424  TGTGGCTCTTCTATCTCCCACTCAAAAGCGGTGAGCGAGCAGACAGCGTC---GGGCTC 480
D 424  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1100  LysGlyIlePheIleLysGlnValLeuGluAspSerProAlaGlyLysThrAsnAlaLeu 1119
QY 481  CAGGTAGGGAGAGATCTCGGATCAATGATATCCATCTCTCTGTTACCCATGAG 540
D 481  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1120  LysThrGlyAspLysIleLeuGluValSerGlyValAspLeuGlnAsnAlaSerHisSer 1139
QY 541  GAGGTCACTCACTCATTCGAACCAAG---AAAACGTGTCTCCATCAAGCTGAGACACATC 597
D 541  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1140  GluAlaValGluAlaIleLysAsnAlaGlyAsnProValIlePheIleValGlnSerLeu 1159
QY 598  GGC-----CTGATCCCGCGGAAAGCTCTCTGATGAGCCCTCACTTGGCAG 645
D 598  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1160  SerSerThrProArgValIleProAsnValHisAsnLysAlaAsnLysIleThr---Ser 1178
QY 646  TATGTGATCAGTTGTGCGAATCTGGGGCGGTGCGAGGCGAGCGCTGGCTCCCTCT--- 702
D 646  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1179  AsnGlnAsnGlnAspThrGlnGluLysLysGluLysArgGlnGlyThrAlaProPro 1198
QY 703  -----GGAATCGGAAACAGGAGAG 726
D 703  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1199  MetLysLeuProProTyrIysAlaLeuThrAspAspSerAspGlnAsnGluGlu 1218
QY 727  AAGGTCTTC-----ATCAGCTGTGAGGC----- 750
D 727  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1219  AspAlaPheThrAspGlnLysIleArgGlnArgTyrAlaAspLeuProGlyGluLeuHis 1238
QY 751  -----TCCCGAGGCGTGTGCTGCGAGCATTTCCAGCGGCGCCCATC 789
D 751  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1239  IleIleGluLeuGluLysAspLysAsnGlyLeuGlyLeuSerLeuAlaGlyAsnLysAsp 1258
D 1239  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

QY 790  CAG---AAGCCTGGCATCTTTATCAGCCATGTAAACCT---GGCTCCCTGTCTCTGTGAG 843
D 790  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1259  ArgSerArgMetSerIlePheValValGlyIleAsnProGluGlyProAlaAlaAsp 1278
QY 844  GTGGATTGGAGATAGGGACACAGATTGTGCAAGTCAATGCGTCGACTTCTTCAACCTG 903
D 844  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1279  GlyArgMetHisIleGlyAspGluLeuLeuGluIleAsnAsnGlnIleLeuTyrGlyArg 1298
QY 904  GATCAACAGGAGGCTGTAATGTGTGTAATAATACCCGACCTGACCATCTCCATTGTA 963
D 904  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1299  SerHisGlnAsnAlaSerAlaIleIleLysThrAlaProSer----- 1312
QY 964  GCTGCAGCTGGCGCGGAGCTGTTTCATGACAGACCCGGAGCGCTGTCGACAGCGCGGAG 1023
D 964  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1313  -----LysValLysLeuValPheIleArgAsn 1321
QY 1024  COTGAGCTGCAGCGCAGGAGCTTCTATGTCAGAGAGCGCTGCGCATGAGTCCCAACAG 1083
D 1024  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1322  GluAspAlaValAsnGlnMetAlaValThrProPheProValProSerSerProSer 1341
QY 1084  ATCTCTCAGGAGCAGCAG-----GAGATGGAGCGGCAAGGAGAAAGAA 1128
D 1084  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1342  SerIleGluAspGlnSerGlyThrGluProIleSerSerGluGluAspGlySerLeuGlu 1361
QY 1129  ATTGCCCAAGAGCAGCAGGAGGAAATGAGAGATACCCGAAAGAGATGGAGAACAGATTGTA 1188
D 1129  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1362  ValGlyIleLysGlnLeuProGluSerGluSerPheLysLeAlaValSerGlnMet--- 1380
QY 1189  GAGGAGGAAGAAATTTAAGAACCAATGGGAAGAACTG-3GGCTCAAGGAACAGCTA 1248
D 1189  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1381  ---LysGlnGlnLysTyr----- 1385
QY 1249  CTCCTTGCCTAAACCATCACTCCTCAGGTACACCCAGTACACCTGTCGCAAGCCAAAGTGA 1308
D 1249  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1386  ---ProThrLysValSerPheSerSerGlnGluIleProLeu-AlaProAlaSerSe 1403
QY 1309  TTTCGGAAATATGAGGAAGGCTTTGACCCCTCTCTATCTTCT--- 1351
D 1309  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1403  rTyrHisSerThrAspAlaAspPheThrGlyTyrGlyGlyPheGlnAlaProLeuSerVa 1423
QY 1352  -----ACCCAGAGCAGATCATGGGAAGAGATGTCGCGCTCTACGCATCAAGAA 1401
D 1352  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1423  IAspProAlaThrCysProIleValProGlyGlnGluMetIleIleGluIleSerLysG 1443
QY 1402  GGAGGATCTTAGACCTGGCCCTGGAAGCGGTGTGGACTCCCCATTTGGGAAGTGTG 1461
D 1402  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1443  YArgSerGlyLeuGlyLeuSerIleValGlyLysAspThrProLeuAsnAlaIleVa 1463
QY 1462  CTTTTCTGTGTGTATGAGCGGAGCTGCTGAGCGCATGCTGGCATTTGTGAAAGGGGA 1521
D 1462  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1463  IleHisGluValTyrGluGluGlyAlaAlaAlaAlaArgAspGlyArgLeuTrpAlaGlyAs 1483
QY 1522  CGAGATCATGGCAATCAACGGCAAGATTGTGACAGACTACACCTGGCTGAGGCTGACGC 1581
D 1522  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1483  pGlnIleLeuGluValAsnGlyValAspLysArgAsnSerHisGluGluAlaIleth 1503
QY 1582  TCCTCTGACAGAGGCTTGAATCAGGCGGGGAGCTGGATCGACCTGTGTGTTCCCTCTG 1641
D 1582  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1503  rAlaLeuArg-----GlnThrProGlnLysValArgLeuValVal- 1516
QY 1642  CCCCCCAAGAGTATGACGATGAGTGCACCTCTTGTG----- 1678
D 1642  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1517  -----TyrArgAspGluAlaHisTyrArgAspGluGluAsnLeuGluIlePh 1532
QY 1679  -----CTGAAGTCCAAAAGGGGA----- 1696
D 1679  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1532  eProValAspLeuGlnLysLysAlaGlyArgGlyLeuGlyLeuSerIleValGlyLysAr 1552
QY 1697  -----AACCAATTCCCGTTAGGAAACAGGTGAGTCCCGCC 1734
D 1697  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
D 1552  gAsnGlySerGlyValPheIleSerAspIleValLysGlyGlyAlaAlaAspLeuAspG 1572
D 1552  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```







```

Db 456 AspAlaGlnGlnProThrGlyProSerValLeuAlaAlaAlaMetValHisGly 475
QY 1240 GAACAGCTACTCTTGGCTAAACCATCATCTGCTAGGTACACCCAGTACCCCTTCCGCAAG 1299
Db 476 AlaSerSerProThrProProAlaAlaThrSerAsnIleThrProLeuProThrAlaAla 495
QY 1300 CCA 1302
Db 496 Pro 496
RESULT 7
US-09-949-016-9470
; Sequence 9470, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9470
; LENGTH: 1771
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9470

Alignment Scores:
Pred. No.: 3-73e-11 Length: 1771
Score: 232.00 Matches: 144
Percent Similarity: 38.63% Conservative: 116
Best Local Similarity: 21.40% Mismatches: 236
Query Match: 5.82% Indels: 177
DB: 4 Gaps: 31

US-09-502-945-5 (1-2162) x US-09-949-016-9470 (1-1771)
QY 310 GTGGAATATGATCAGTACCCCGG-----CGTCCAGGAAGCTGAAGAG 357
Db 19 LeuGluArgAspLysMetSerAlaArgAlaAlaAlaLysSerThrAlaMetGluGlu 38
QY 358 -----GTGCGTCTGGACCGCTGCACCCCGAAGGCTCGGC 393
Db 39 ThrAlaIleTrpGluGlnHisThrValThrLeuHisArgAlaProGlyPheGly 58
QY 394 CTGAGTGTGCGTGGCTGCTGAG-----TTTGGCTGTGG-----CTCTTC 435
Db 59 IleAlaIleSerGlyGlyArgAspAsnProHisPheGlnSerGlyGluThrSerIleVal 78
QY 436 ATCTCCCACTCATCAAGCGGTGACGAGCAGCGTCCGGCTCCAGGTAGGGGACGAG 495
Db 79 IleSerAspValLeuLysGlyGlyProAlaGluGly---GlnLeuGlnGluAsnAspArg 97
QY 496 ATCTGCGGATCAATGGATATTCCATCTCTCTGTACCCATGAGGAGTCAACCTC 555
Db 98 ValAlaMetValAsnGlyValSerMetAspAsnValGluHisAlaPheAlaValGlnGln 117
QY 556 ATTCTGA---ACCAAGAAATGCTGTCCATCAAGATGACACATCGC-----CTGATC 606
Db 118 LeuArgLysSerGlyLysAsnAlaLysIleThrIleArgArgLysLysValGlnIle 137
QY 607 CCGGTGAAAGTCTCTCTGATGAGCCCTCACTTGGCAGTATGTGATCAGTTTGTGCG 666
Db 138 ProValSerArgProAspProGluProValSerAspAsnGluGluAspSerTyrAspGlu 157
```

```

QY 667 GAATCTGGGGCGTGCAGGAGCCCTGGCTCCCTCGAAATCGGAAACCAAGAG--- 723
Db 158 GluIleHisAspProArgSerGlyArgSerGlyValValAsnArgArgSerGluLysIle 177
QY 723 -----
Db 178 TrpProArgAspArgSerAlaSerArgGluArgSerLeuSerProArgSerAspArgArg 197
QY 724 -----NAGAAGGTCTTCATCA3CTGGTAGGCTCCCGA--- 756
Db 198 SerValAlaSerSerGlnProAlaLysProThrLysValThrLeuValLysSerArgLys 217
QY 757 -----GGCCTTGGCTGCAGCATTTCCAGCGCCCATCCAGAACGCTGGCATCTTTATC 810
Db 218 AsnGluGluTyrGlyLeuArgLeuAlaSer-----HisIlePheVal 231
QY 811 AGCCATGTGAACCTGGCTCCCTGTCTGTAGGTGGGA---TTGGAGATAGGGACCAAG 867
Db 232 LysGluIleSerGlnAspSerLeuAlaAlaArgAspGlyAunIleGlnGluGlyAspVal 251
QY 868 ATTGTGGAAGTCAATGGCGTGCAGCTCTCTACCTGGATCAACAGAGGCTGTAATGTG 927
Db 252 ValLeuLysIleAsnGlyThrValThrGluAsnMetSerLeuThrAspAlaLysThrLeu 271
QY 928 CTGAAAAATAGCGCAGCGCTGACCATCTCCATTGTAGCTGCAGCTGGCGCGAGCTGTT 987
Db 272 IleGluArgSerLysGlyLysLeuLysMetValValGlnArgAspGluArgAlaThrLeu 291
QY 988 ATG-----ACAGCCGGGAGCGG 1005
Db 292 LeuAsnValProAspLeuSerAspSerIleHisSerAlaAsnAlaSerGluArgAspAsp 311
QY 1006 CTGGCAGAG----- 1014
Db 312 IleSerGluIleGlnSerLeuAlaSerAspHisSerGlyArgSerHisAspArgProPro 331
QY 1015 -----GCGCGGCGAGCTGAGCTG--CAGCGGCGAGGAGCTTCTCATGCAGAAAGCGGCTG 1065
Db 332 ArgArgSerArgSerArgSerProAspGlnArgSerGluProSerAspHisSerArgHis 351
QY 1066 GCGATGGAG-----TCCAACAAGATCTCTCAGGAGCAGCA3GAGATGAGCGGCAAGG 1119
Db 352 SerProGlnGlnProSerAsnGlySerLeuArgSerArgAspGluGluArgIleSerLys 371
QY 1120 AGAAAAGAAATTGCCAGACGACAGGAGGAAATGAGAGATACCGGAGAGAGATGGAA 1179
Db 372 ProGlyAlaValSerThrProValLysHisAlaAspAspHisThrProLysThrValGlu 391
QY 1180 CAGATT---GTAGAGGAGAGAGAAAGTTTAAGAAGCAATGCGAAGAAGACTGGGGCTCA 1236
Db 392 GluValThrValGluArgAsnGlnLysGlnThrProSerLeuProGlu----- 407
QY 1237 AAGGAACAGCTACTCTTGCCTAAACCATCATCTGCTGAGGT3CACCCAGTACCCCTCGC 1296
Db 408 -----ProLysProValTyrAlaGlnValGlyGln----- 417
QY 1297 AAGCCAAAGTATTTCGGAATATGAGAGGCTTTGACCCCTACTCTATGTTTACCCCC 1356
Db 418 -----ProAspValAspLeuProValSerProSerAspGlyValLeuPro 432
QY 1357 AGAGCAGATCATGGGAAGGATGTC-----CG3CTCTACGCATCAAGAA 1401
Db 433 AsnSerThrHisGluAspGly-IleLeuArgProSerMetLysLeuValLysPheArgLys 452
QY 1402 GGAGGGATCTTTAGACCTGGCCCTCGAAGCGGCTGGAGCTCCCCATTGGGAAGGTGT 1461
Db 452 sclyAspSerValGlyLeuArgLeuAlaGlyLysAsnAsp-----ValGly---IlePhe 469
QY 1462 CGTTTCTGCTGTATGATGAGCGGAGCTGCTGAGCGGAGTGGTGGCATTGTGAAAGGGA 1521
Db 469 eValAlaGlyValLeuGluAspSerProAlaAlaLysGlu---GlyLeuGluGluGlyAs 488
```



```
QY 1522 CGAGATCATGGCAATCAACGGCAAGATTGTGACAGACTACACCTCGCTGAGGCTGACGC 1581
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
488 pGin1leLeuArgValAsnAsnValAspPheThrAsn1le1leArgGluGluAlaValle 508
QY 1582 TGCCCTGCGAGAAGCCCTGGAAATCAGGCGGGGACTGATCGACTTGTGTGCTGCTG 1641
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
508 uPheLeu-----LeuAspLeu----- 513
QY 1642 CCCCCCAAGAGTATGACGATGAGCTGACCTTCTTCTGTAAGTCCAAAAGGGGAAACCA 1701
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
514 ----ProLys-----GlyGluGluValThr1leLeuAlaGlnLysLys----- 527
QY 1702 AATTCAGCGCTTAGGAACAGTACGCTCGGCCCCCACCCTCGTGAACACAAAGCCTCGAC 1761
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
528 -----AspValTyArgArg1leValGluSerAspValGlyAs 540
QY 1762 CAGCCTTGAG---AGAGGCCACATGACACACACAGATGCGATCCTTGGGACCTGAATCT 1818
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
540 pSerPheTyrlleArgThrHisPheGluTyGluLysGluSerProtyrGly----- 557
QY 1819 ATCACCAGGAATCTCAAACTCCCTTTGGCCCTGAACCCAGGGCCAGATAAGGAACACGCTC 1878
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
558 -----LeuSerPheAsnLysGlyGluValPheArgValVa 569
QY 1879 GGCCCACTTTTGAAGGCCAATGTGAGGAAGGGAGCAGCCGCTTGTGGAGAAGA 1938
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
569 lAspThrLeuTyAsnGlyLysLeu---GlySerTrpLeuAla1leArg1leGlyLysAs 588
QY 1939 TCTCAAGGATCCAGACTCTCATCTCTTCTCT-----CTGGCCCA 1977
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
588 nHisLysGluValGluArgGly1le1leProAsnLysAsnArgAlaGluGlnLeuAlaSe 608
QY 1978 GTGAATTTGGTCTCTCCCA-----GCTTTGGGGGAC 2008
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
608 rValGlnTyThrLeuProLysThrAlaGlyGlyAsp 620
```

## RESULT 8

```
US-09-562-737-21
; Sequence 21, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UTSW0708
; CURRENT APPLICATION NUMBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-562-737-21
```

```
Alignment Scores:
Pred. No.: 3,7e-11 Length: 724
Score: 229.50 Matches: 146
Percent Similarity: 37.54% Conservative: 101
Best Local Similarity: 22.19% Mismatches: 204
Query Match: 5.75% Indels: 207
DB: 4 Gaps: 35
```

US-09-502-945-5 (1-2162) x US-09-562-737-21 (1-724)

```
QY 340 TCCAGGAAGCTGAAGAGGTGCTCTGGACCGTCTGCACCCCGAAGGCTCGGCTGAGT 399
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
155 AlaGluVal1le1leGlu1leLysLeuLys---GlyProLysGlyLeuGlyPheSer 173
QY 400 GTGCGTGGTGGC-----CTGGAGTTTGGTGTGGCTCTTCATCTCCAC 444
```

```
Db |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
174 IleAlaGlyGlyValGlyAsnGlnHis1leProGlyAspAsnSer1leTyValThrLys 193
QY CTCATCAAAAGGGGTGAGGACAGACGCTCGGG---CTCAGGTAGGGACGACGATCGTC 501
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
194 Ile1leGluGlyGlyAlaAlaHisLysAspGlyArgLeuGln1leGlyAspLys1leLeu 213
QY CGGATCAATGGATATTCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 561
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
214 AlaValAsnSerValGlyLeuGluAspValMetHisGluAspAlaValAlaLeuLys 233
QY ---ACCAAGAAACTGTGTCATCAAGTG-----AGACACATCGGCTGATCCCC 609
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
234 AsnThrTyAspValValTyLeuLysValAlaLysProSerAsnAlaTyLeuSerAsp 253
QY GTGAAAGAGCTCTCTCATGAGCCCTCACTTGG---CAGTATGTGTGATCAGTTTGTGTG 666
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
254 SerTyAlaProProAsp1leThrSerTySerGlnHisLeuAspAsnGlu1leSer 273
QY GAATCTGGGGGCGTGGCAGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 696
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
274 HisSer-----SerTyLeuGlyThrAspTyProThrAlaMetThrProThr 289
QY ---TCCCTCGAAATCGGAA-----AACAG 720
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
290 SerProArgArgTySerProValAlaLysAspLeuLeuGlyGluGluAsp1leProArg 309
QY GAGAAAGAGCTCTCTCATGAGCCCTCGGCTAGGCTCCCGAGGCTTGGCTGCGACATTTCCAGC 780
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
310 GluProArgArg1leVal1leHisArgGlySerThrGlyLeuGlyPheAsn1leValGly 329
QY GSCCCCATCCAGAGCTGGCATCTTTATCAGCCATGTG-----AACTCGCTCC 831
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
330 GlyGlu---AspGlyGluGly1lePhe1leSerPhe1leLeuAlaGlyGlyProAlaAsp 348
QY CTGCTCTGCTGAGGTGGATTGAGATAGGGGACGAGATTGTCGAACTCAATGCGCTCGAC 891
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
349 LeuSerGlyGlu-----LeuArgLysGlyAspGln1leLeuSerValAsnGlyValAsp 366
QY TTCTCTAACTGGATCACAAAGGAGCTGTAAATGTCTGCTGAAAAAATAGCCGACCTGACC 951
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
367 LeuArgAsnAlaSerHisGluGlnAlaAla1leAlaLeuLysAsnAla---GlyGlnThr 385
QY ATCTCATTTGATGTGACGCTGCGCGGAGCTGTTTCATGACAGACCGGGAGCGGTGGCA 1011
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
386 ValThr1le1leAlaGln-----TyLysProGluGluTySerArgPhe 400
QY GAGGCGCGCAGCTGAGCTGCGCGGAGGAGCTTCTCATGACAGAGCGGCTG----- 1065
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
401 GluAlaLys1leHisAspLeuArgGluGln-----LeuMetAsnSerSerLeuGlySer 418
QY ---GCGATGGAGTCCAAC----- 1080
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
419 GlyThrAlaSerLeuArgSerAsnProLysArgGlyPheTyrlleArgAlaLeuPheAsp 438
QY ----- 1080
Db ----- 1080
QY TyAspLysThrLysAspCysGlyPheLeuSerGlnAlaLeuSerPheHisPheGlyAsp 458
QY -----AGATCTCCAGGACGAGGAGATGGAGCGGCAAGGAGAAAGAAATGGC 1134
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
459 ValLeuHisVal1leAspAlaSerAspGluGluTyTrpGlnAlaArgValHisSer 478
QY CAGAAAGCAGCAGGAGGAAATGAGAGATACCGGAGGAGATGGAACAGATGTGTAGAGGAG 1194
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
479 AspSerGluThrAsp-----Asp1leGlyPhe1leProSerLys 491
QY GAAGAGAAGTTTAAAGAACATGGAA-----GAAGACTGGGCTCA----- 1236
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
492 ArgArgValGluArgArgGluTrpSerArgLeuLysAlaLysAspTrpGlySerSer 511
QY -----AAGAAACAGCTACTCTTGGCTTAAACCCATCACT---GCTGAGGTA 1278
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```



Db 290 gSerHisAspArgProProArgArgSerArgSerArgSerProAsp----- 305  
QY 1177 GAACAGATTGTAGAGAGGAAGAGAGTTTAAAGAACAAATGGGAAGAGAGCTGGGGCTCA 1236  
Db 306 -----GlnArgSerGluProSerAspHisSerArgHisSerProGly 319  
QY 1237 AAGGAACACTACTCTTGGCTA-----AAACATCACT 1269  
Db 319 ngInProSerAsnGlySerLeuArgSerArgAspGluGluArgIleSerLysProGlyAl 339  
QY 1270 GCTGAGGTACACCC-----AGTACCCTCTCGCAAGCAAAAGTGATT 1311  
Db 339 aVal-SerThrProValLysHisAlaAspAspHisThrProLysThrValGluGluVal 359  
QY 1312 CCGAAATATGAGGAAGGCTTTGACCCCTACTCTATGTTTCAACCCAG----- 1358  
Db 359 hrValGluArgAsnGlyLysGlnThrProSerLeuProGluProLysProValTyrAlaG 379  
QY 1359 -----AGCAGATCATGGG----- 1372  
Db 379 lnValGlyAsnGlnMetTrpIleTyrLeuSerValHisLeuMetValSerTyrLeuIleG 399  
QY 1373 -----AAGGATGTCGGGCTCTACGCATCAAGAGAGGAGG 1406  
Db 399 lnLeuMetLysMetGlyPheLeuArgProSerMetLysLeuValLysPheArgLysGlyA 419  
QY 1407 GATCTTACAGCTGGCCCTGGAGGCGGTGTGGACTCCCCCATTTGGGAAGGTGTCGTTT 1466  
Db 419 spSerValGlyLeuArgLeuAlaGlyLysAsnAsp-----ValGly-----IlePheValA 436  
QY 1467 CTGCTGTGTATAGCGGGAGCTGTGAGCGGCATGTGTGCATTTGTAAGGGAGCAGA 1526  
Db 436 laGlyValLeuGluAspSerProAlaAlaLysGlu---GlyLeuGluGluGlyAspGlnI 455  
QY 1527 TCATGCCAATCAAGCGCAAGATTGTGCACAGACTTACACCCCTGGCTGAGGCTGACGTCGCC 1586  
Db 455 leuLeuArgValAsnAenValAspPheThrAsnIleleArgGluGluAlaValLeuPheLe 475  
QY 1587 TGCAGAAGCGCTGGAATCAGGGCGGGAGCTGGATCGACCTTGTGTGCTGCGCTGCCCCC 1646  
Db 475 eu-----LeuAspLeu-----P 479  
QY 1647 CAAAGAGTATGACGATGAGCTGACCTTCTGTGAAGTCCAAAGAGGGGAAACCAATTC 1706  
Db 479 roLys-----GlyGluGluValThrIleLeuAlaGlnLysLys----- 492  
QY 1707 ACGCTTGAGGAACAGTGAAGCTCGGCCCCCACTCGTGAACACAAAGCCTCGGACCGACC 1766  
Db 493 -----AspValTyrArgArgIleValGluSerAspValGlyAspSerP 507  
QY 1767 TTGAG---AGAGGCCACATGACACACACAGATGGCATCTTGGGACCTGGAATCTATCAC 1823  
Db 507 heTyrIleArgThrHisPheGluTyrGluLysGluSerProTyrGly----- 522  
QY 1824 CCAGGAATCTCAAACTCCCTTGGCCCTGAACAGGCGGCAGATAAGAAACAGCTCGGGCC 1883  
Db 523 -----LeuSerPheAsnLysGlyGluValPheArgAlaValAspT 536  
QY 1884 ACTTTTGTGAGCCCAATGTGGNGGAAGGAGCAGCAGCGCTTTGGGAGAGATCTCA 1943  
Db 536 hrLeuTyrAsnGlyLysLeu---GlySerTrpLeuAlaIleArgIleGlyLysAsnHisL 555  
QY 1944 AGGATCCAGACTCTCATCTCTTTCCT-----CTGGCCCACTGAA 1982  
Db 555 ysGluValGluArgGlyIleIleProAsnLysAsnArgAlaGluGlnLeuAlaSerValG 575  
QY 1983 TTTGTTCTCTCCCA-----GCTTTGGGGGAC 2008  
Db 575 lnTyrThrLeuProLysThrAlaGlyGlyAsp 585

RESULT 10

US-09-562-737-28

; Sequence 28, Application US/09562737

; Patent No. 6428967  
; GENERAL INFORMATION:  
; APPLICANT: Herz, Joachim  
; APPLICANT: Gotthardt, Michael  
; TITLE OF INVENTION: LDL Receptor Signaling Pathways  
; FILE REFERENCE: UTSW0708  
; CURRENT APPLICATION NUMBER: US/09/562,737  
; CURRENT FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 132  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 724  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Sequence  
US-09-562-737-28

Alignment Scores:  
Pred. No.: 1,548-09 Length: 724  
Score: 211.00 Matches: 139  
Percent Similarity: 39.74% Conservative: 101  
Best Local Similarity: 23.01% Mismatches: 205  
Query Match: 5.29% Indels: 159  
DB: 4 Gaps: 35

US-09-502-945-5 (1-2162) x US-09-562-737-28 (1-724)  
QY 250 GAACCCAGCGCTCCCTCTGTTTCATGCCATTCGG-----COGCTGATC 294  
Db 107 GlnGlnGlyArgLeuArgValAsnAspSerIleArgPheValAsnGluValAspValArg 126  
QY 295 CCACCTGAACACACAGCTGGAATATGATCAGCTGACGCCCC----- 333  
Db 127 GluSerThrHisSerAlaAlaValGluAlaLeuThrGluAlaGlySerIleValArgLeu 146  
QY 334 -----CGCGCG-----TCCAGGAAGCTGAAGAGGTGGCTCTGGACCGCTCTG 375  
Db 147 TyrTrpMetArgArgLysProAlaGluLysTyrIleGluIleLysLeuLys--- 165  
QY 376 CACCCCGAAGCGCTCGGCTGAGTGTGGCTGGCG-----CTGGAGTTT 420  
Db 166 GlyProAlaGlyLeuGlyPheSerIleAlaGlyLysAspGlyAsnGlnHisIleProGly 185  
QY 421 GGCTGTGGGCTCTTCATCTCCACCTCATCAAGCGGTCCAGCAGACAGCGCTCGG--- 477  
Db 186 AspAsnGluIleTyrValThrLysIleIleGluGlyPheAlaAlaHisLysAspGlyArg 205  
QY 478 CTCAGGTAGGGAGCAGATCGTCCGGATCAATGATATTCATCTCTCTGTACCCAT 537  
Db 206 LeuGlnGlyGlyAspLysIleLeuAlaValAsnSerHisGlyLeuGluAspValMetHis 225  
QY 538 GAGGAGGTCACTCACTCATTCGA---ACCAGAAAACCTGTCTCCATCAAGTACAGACAC 594  
Db 226 GluAspIleValAlaAlaLeuLysAsnThrTyrAspLysValTyrLeuLysValAlaLys 245  
QY 595 ATCGGCTCATCCCGTGAAGAGCTCT-----CTGTAGTGGCCCTCACT-----TGG 642  
Db 246 ProSerLeuAlaTyrLeuSerAspSerTyrAlaProMetAspIleThrThrSerTyrSer 265  
QY 643 CAGTATGTGGATCAGTTTGTTCGGAATCTGGGGCGTCCGAGGCGCAGC----- 690  
Db 266 GlnHisAsnAspAsnGluIleSerHisSer---SerTyrGlnGlyThrAspTyrProThr 284  
QY 691 -----CTGGGCTCCCTCGGAATCGGAA----- 714  
Db 285 AlaMetThrArgThrSerProArgArgTyrSerProValSerLysAspLeuGlyGlu 304  
QY 715 -----NACAAGGAGGAAGAGGTCTTCATCAGCGCTGTAGGCTCCCGAGGCTTGGC 765  
Db 305 GluAspIleThrArgGluProArgArgIleValIleHisValGlySerThrGlyLeuGly 324



Db 310 GluProArgValIleValIleHisArgGlySerThrGlyTrpGlyPheAsnIleValGly 329  
QY 781 GGGCCCATCCAGAGCGCTGCATCTTTATCAGCCATGTC-----AAACCTGCGTCC 831  
Db 330 GlyGlu---AspTyrGluGlyIlePheIleSerPheIleLeuAspGlyGlyProAlaAsp 348  
QY 832 CTGCTGCTGAGGTGGATGGAGTAGGGACAGATTGTCGAAGTCAATGGCTCGAC 891  
Db 349 LeuSerGlyGluGlu-----ArgTysGlyAspGlnIleLeuSerValPheGlyValAsp 366  
QY 892 TTCTCTAACTGGATCACAAGAGGCTGTAAATGTGCTGAAAAATAGCGCGAGCTGACC 951  
Db 367 LeuArgAsnAlaSerHisGlyGlnAlaAlaIleAlaLeuIleYAsnAlaHisGln---Thr 385  
QY 952 ATCTCATTTAGCTCAGCTGCGCGAGCTGTTTCATCAGACAGCGGAGCGGTGGCA 1011  
Db 386 ValThrIleIleAlaGln-----TyrIleProGluGluTyrSerArgPhe 400  
QY 1012 GAGGCGCGCAGGCTGAGCTGCAGCGGCGAGGAGCTTCTCATGACAGAGCGGTGGCGATG 1071  
Db 401 GluAlaLeuIleHisAspLeuArgGluGlnLeuMetMetSerSerLeuGlySerGlyThr 420  
QY 1072 GAGTCCAAACAAGATCTCCAGGAGCAGCAGGAGATGGAGCGCAAGAGGAGAAAGAAAT 1131  
Db 421 AlaSerAsnArg-----SerAsnProTysArgGlyPhe 431  
QY 1132 GCCCAGAGCGCAGCAGAGGAAATGAGATACCGGAAG----- 1170  
Db 432 TyrGlnArgAlaLeuPheAspTyrAspTyrAspThrArgAspCysGlyPheLeuSerGlnAla 451  
QY 1170 ----- 1170  
Db 452 LeuThrPheHisPheGlyAspValLeuHisValAlaSerAspGluTrpTrp 471  
QY 1171 GAGATGGAACAGATTCTAGCAGGAGGAGAGAGATT----- 1206  
Db 472 GlnTrpArgArgValHisSerAspSerGluThrTyrAspIleGlyPheIleProSerLys 491  
QY 1207 -----AAGAAGCAATGGGAA-----GAAGACTGGGGCTCA----- 1236  
Db 492 ArgAlaValGluArgArgGluTrpSerArgLeuAspAlaLysAspTrpGlySerSer 511  
QY 1237 -----AAGAAGCAGCTACTCTTGCCTTAAACCTACT---GCTGAGGTA 1278  
Db 512 GlyGluGlnGlyArgGluAspSerValLeuSerPheGluThrValThrGlnMetGluVal 531  
QY 1279 CACCCAGTACCCCTTCGCAAGCCAAAGTATTCGCGAATATGAGGAAGGCTTTGACCC 1338  
Db 532 HisGlyAlaArg-----Pro 536  
QY 1339 CTACTCTATGTTTACCCAGCAGATCATGGGGAAGGATGTCCGCGCTCTAGCATCAA 1398  
Db 537 IleIleIleLeuGlyProHisLysAspArgala----- 547  
QY 1399 GAAGAGGAGATCTTACAGCTGCGCTGGAAGCGGTGTGGACTCCCCCATTTGGGAAGT 1458  
Db 548 AsnAspAspLeuIleLeuGluPheProAspLys----- 558  
QY 1459 GGTGCTTTCTGCTGTATGAGCGGCGAGCTGCTGAGCGCATGGTGCGATTGTGAAGG 1518  
Db 559 -----PheGlySerCys-LysProHisThrArgProLys 571  
QY 1519 GGACGAGATCATGGCAATCAACGGCAAGATTGTGACAGACTACACCTGGCTGAGGCTGA 1578  
Db 571 gglu-----LeuGluIleAspGlyArg-----AspTyrHisPheMetSerSer 586  
QY 1579 CGCTGCCCTGCAGAAAGCGCTTGAATCAGGCGGGGAGTGGATCGACCTTGTGGTCCCT 1638  
Db 586 gGluLysMetGluLys----- 591  
QY 1639 CTGCCCCCAGAGGATATGACGATGAGCTGACCTTCTTCTGCTGAAGTCCAAAGGGAAA 1698  
Db 592 -----AspAsnGlnAlaHisLysPheIleGluAlaGlyArgTyrAs 605

QY 1699 CCAATTACCGCTTAGGAAACAGT-----GAGCTCGGCC 1734  
Db 605 nSer---HisLeuTyrGlyThrSerSerGlnSerValArgGluValAlaGluGlnThrLy 624  
QY 1735 CCACCTCGTGAACACAAAGCCTCGGACAGCCTTGAGAGAGGCCACATGACACACACCAG 1794  
Db 624 shiCysIleLeuAspValSerAlaValAlaValArgLeuGlnAlaHis----- 642  
QY 1795 ATGGCATCTTGGGACCTGAATCTATCACCAGGAATCTCAAACTCCCTTTGGCCCTGAA 1854  
Db 643 -TrpHisProIleAlaIlePheIleArgProTyrSerLeuGluAsnValLeuGluIleAs 662  
QY 1855 C-----CAGGGCCAGATAGGAACACAGCTCGGGCCACTTTTGAAG- 1895  
Db 662 nAlaArgIleThrGluGluGln-AlaArgLysAspPheAspArgAlaThrLysLeuGluG 682  
QY 1896 -----GCCAATGTGAGGAAAGGAGGAGCAGCGCTTTGGG 1932  
Db 682 InPhePheThrGluCysPheSerAlaIleValGlyGlyAspSerPheGluGluIleTyrH 702  
QY 1933 AGAAGATCTCAAGGATC-----CAGACTCTCATCTTCTCTCTGG 1973  
Db 702 ishivallysargValIleGluAspLeuSerIleProTyrIleTrp 717

RESULT 12

US-09-045-632-50  
; Sequence 50, Application US/09045632  
; Patent No. 6001575  
; GENERAL INFORMATION:  
; APPLICANT: HUGANIR, RICHARD L.  
; APPLICANT: DONG, HUALING  
; TITLE OF INVENTION: THERAPEUTIC USES OF GRIP AND  
; TITLE OF INVENTION: GRIP-RELATED MOLECULES  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSES: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/045,632  
; FILING DATE: 19-MAR-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/041,016  
; FILING DATE: 19-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Corleiss, Peter F.  
; REGISTRATION NUMBER: 33,860  
; REFERENCE/DOCKET NUMBER: 48147/1699-CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1050 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-045-632-50  
  
Alignment Scores: 4.7e-09 Length: 1050  
Pred. No.: 206.50 Matches: 169  
Score:



```
QY 1939 TCTCAAGGATCCAGACTCTCATCTTCTCTGCGCCAGTGAATTTGGTCTCTCCAGC 1998
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 712 uproPheAppPro-IleIleIleSerGlyLeu-----ThrLysArgGlyLeuAlaGluA 730
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 1999 TTTGGGGGACTCTCTCTTCAACCCCTAATAAGACCCCACTGGAGTCTCTCTCTCTCCATC 2058
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 730 rgThrGlyAlaSerMetLeuGlyThAlaTyTrpProSer***SerValSerLeuLysG 750
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 2059 CCTCTCTCTGCGCTCTGCTCTCTAATTTGCTGCCAGGATTTGCTCAACACTTACTCTG 2117
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 750 lyArgProLeuSerGluAlaIleHisLeuLeuGlnValAlaGlyGluThrValThrLeu 769
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 13
US-09-080-855-12
; Sequence 12, Application US/09080855A
; Patent No. 6083721
; GENERAL INFORMATION:
; APPLICANT: Saraz, Jan
; APPLICANT: Franz, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Genez, Leonel Jorge
; APPLICANT: Heidin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/080, 855A
; EARLIER FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: 08/805, 583
; EARLIER FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-080-855-12

Alignment Scores:
Pred. No.: 1,15e-08 Length: 2466
Score: 204.50 Matches: 143
Percent Similarity: 36.35% Conservative: 94
Best Local Similarity: 21.93% Mismatches: 214
Query Match: 5.13% Indels: 201
DB: 3 Gaps: 29

US-09-502-945-5 (1-2162) x US-09-080-855-12 (1-2466)
QY 1 CTGGCGCGGTCCGGTCCGGCTCTT----- 27
||| ||| ||||| |||
Db 991 ProProGlnThrValAlaGluLeuValGlyLysProSerHisGlnMetSerArgSer 1010
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 28 ---TCCAGTCTCTGGCAGCGGCGCCGACCCGAGGACGGTCTGTCGCAACGCCAGCTGGA 84
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1011 AspAlaGluSerLeuAlaGlyValThrLysLeuAsnSerLysSerValAla----- 1028
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 85 CTGGCGCCAGCATGACGACGAAAGTGGCCCGAGAATTCGGGATAAGTGGAATTTCTG 144
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1029 -----SerLeuAsnArgSerProGluArg---LysHisGluSerAspSerSer 1044
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 145 ATTGAAATGATGACAGAGAGGCTATCTCTATGATGTGCTGGAATGTACCAACGACCC 204
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1045 SerIleGluAspProGlyGlnAlaTyrrValLeuAspValLeu-----HisLysArg 1061
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 205 ATGGAGTGGCGGTCTGCTGGGAGACCTGAAGCTGTCATCAATGAACCCAGCGCTG 264
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1062 TrpSer-----IleValSerSerProGluArg--- 1070
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 265 CCTCTGTTGATGCCATTGGCGCGCTGATCCCACTGAAGCACCAGGTGGAATATGATCAG 324
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1071 -----GluIleThrLeuValAsnLeuLysLysAspAlaLysTyrr----- 1083
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 325 CTGACCCCCCGCGCTCCAGGAGCTGAAAGGAGGTGCGTCTGGACCGTCTGCAACCCCGAA 384
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
```

```
1083 ----- 1083
385 GGCTCGGCTCAGTGTGGTGGTGGCTGGAGTTTGGC-----TGTGGCTCTTC 435
||| ||| ||||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1084 GlyLeuGlyPheGlnIleIleGlyGlyGlyLeuMetGlyArgLeuAspLeuGlyIlePhe 1103
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 436 ATCTCCCACTCATCAAGCGGTGAGGACAGCAGCGTCGG---CTCCAGGTAGGGAC 492
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1104 IleSerSerValAlaProGlyGlyProAlaAspPheHisGlyCysLeuLysProGlyAsp 1123
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 493 GAGATCGTCCGATCAATGATATTCATCTCTCTCTGTTACCCATGAGGAGGTCATCAAC 552
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1124 ArgLeuIleSerValAsnSerValSerLeuGluGlyValSerHisHisAlaIleGlu 1143
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 553 CTCATTGCAACCAAGAAACTGTGTCCATCAAAAGTGAGACACATCGGCTGATCCCGTG 612
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1144 IleLeu----- 1145
613 AAAGCTCTCTGATGAGCCCTCACTTGGCAGTATGTGATCAGTTTGTGTCGAATCT 672
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1146 GlnAsnAlaProGluAsp-----ValThrLeuValIleSerGlnPro 1159
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 673 GGGGGCTCGAGGACGCTGGGCTCCCTGGAAATCGGGAACCAAGAGAGAGAGGTC 732
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1160 -----LysGluLys----- 1162
733 TTCATCAGCTGTAGGCTCCGAGCGCTTGGCTGCAGCATTTCCAGCGGCCCATCCAG 792
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1163 ---IleSer-----LysValProSerThrProValHis 1172
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 793 AAGCTGGCATCTTTATCAGCCATGAAACCTGGCTCCCTGTCTGTCTGAGGTGGGATTG 852
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1173 LeuThrAsnGluMetLysAsnTyrrMetLysLysSerSer----- 1185
853 GAGATAGGGGACCATGTTCTCGAAGTCAATGGCTGACTTCTCTAACTGGATCAACAG 912
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1186 -----TyrMetGlnAspSerAlaIleAspSerSerLysAspHisHis 1200
913 GAGGCTGTAAATGTCTGAAATAATAGCCGACGCTCACCATCTCCATTGTAGTGCAGCT 972
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1201 TrpSerArgGlyThrLeu-----ArgHisIleSerGluAsnSerPheGlyProSer 1217
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 973 GGC-----CGGAGCTGTTCATGACAGACCGGAGCGGCTGCGACAGCGCGCAGCGT 1026
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1218 GlyGlyLeuArgGluGlySerLeuSerSerGlnAspSerArgThrGluSer-AlaSerLe 1237
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 1027 GAGCTGCAGC-----GGCAGGAGCTTCTCATGTCAGAACGGC-----TGGCGATG 1071
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1237 userGlnSerGlnValAsnGlyPhePheAlaSerHisLeuGlyAspGlnThrTrpGlnG 1257
1072 GAGTCCAAACAGATCTCCAGGAGCAGCAGGAGATGGAGCGGCAAGAGGAGAGAAAT 1131
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1257 user-GlnHisGlySerProSerProSerValIleSerLysAlaThrGluLysGluThrp 1277
1132 GCCCAGAGGACGACGAGGAGAAATGAGATACCGGAA---GGAGATGAACAGATTGT- 1187
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1277 heThrAspSerAsnGlnSerLysThrLysLysProGlyIleSerAspValThrAspTyrs 1297
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 1188 -----AGAGGAGAGAGAGAGTTTAAGAGCAATGGGAAGACACTGGGGCTCAAGAGAA 1242
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1297 erAspArgGlyAspSerAspMetAspGluAla----- 1308
1243 CAGCTACTCTTCCCTAAACCATCACTGCTGAGGTACACCCAGTACCCCTTCGCAAGCCA 1302
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1308 hrTy-SerSerSerGlnAspHisGln-----ThrProLysGlnGluSerSerSers 1325
1303 AAGTATTTCCGGAAATATGAGGAAGGCTTTGACCCCTACTCTATGTTTCAACCCAGAGCA 1362
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1325 erValAsnThrSerAsn--LysMetAsnPhelysThrPheSerSerSerProProLysPr 1344
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 1363 GATCATGGGAGGAGGATGTCGGCTCTACGCATCAAGAGAGGAGGATCTCTAGACCTGGC 1422
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
```



Db 1344 o-----GlyAspIlePheGluValGluLeuAlaLysAsnAspSerLeuGlyIleSe 1362  
QY 1423 CTGGAAGCGGTGTGACTCCCCATT-----GGGAAGTGGTGGTCTTCTGCTGTGA 1476  
Db 1362 rValThrGlyValAsnThrSerValArgHisGlyGlyIleTyrValLysAlaVal11 1382  
QY 1477 TGAGCGGGAGGTGCTGAGCGGCATGCTGGCATTTGTAAAGGGGACGAGATCATGGCAAT 1536  
Db 1382 eProGlnGlyAlaAlaGluSerAspGlyArgIleHisLysGlyAspArgValLeuAlaVa 1402  
QY 1537 CAACGGCAAGATTGTACAGACTACACCTGCTGAGCTGAGCTGACGCTGCCCTG----- 1588  
Db 1402 laenGlyValSerLeuGluGlyAlaThrHisLysGlnAlaValGluThrLeuArgAsnTh 1422  
QY 1588 ----- 1588  
Db 1422 rGlyGlnValValHisLeuLeuGluLysGlyGlnSerProThrSerLysGluHisVa 1442  
QY 1589 -----CAGAAAGCGCTGGAATCAGCGGGGGGACTG 1617  
Db 1442 lProValThrProGlnCysThrLeuSerAspGlnAsnAlaGlnGlyProGluLys 1462  
QY 1618 GATCGACCTGTGGTGGCTGTGCCCCCAAGAGGATGAC-----GATGAGCT 1668  
Db 1462 sValLysLysThrThrGlnVal-----LysAspTyrSerPheValThrGluGluAs 1479  
QY 1669 GACCTTC-----TTGCTGAGTCCAAAGGGGAAACCAATTCACGCGTTAGGAAA 1719  
Db 1479 nThrPheGluValLysLeuPheLysAsnSerSerGlyLeuGlyPheSerPheSerArgGl 1499  
QY 1720 CAGTGAGCTCCGGGCCCCACCTCGTGAAC 1747  
Db 1499 uAspAsnLeuIleProGluGlnIleAsn 1508

## RESULT 14

US-09-566-076-12  
; Sequence 12, Application US/09566076  
; Patent No. 6475775  
; GENERAL INFORMATION:  
; APPLICANT: Saras, Jan  
; APPLICANT: Franzn, Petra  
; APPLICANT: Aspenstrm, Pontus  
; APPLICANT: Hellman, Ulf  
; APPLICANT: Gonez, Leonel Jorge  
; APPLICANT: Haldin, Carl-Henrik  
; TITLE OF INVENTION: PARQ, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1  
; FILE REFERENCE: L0461/7030  
; CURRENT APPLICATION NUMBER: US/09/566,076  
; EARLIER FILING DATE:  
; EARLIER APPLICATION NUMBER: 09/080,855  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 2466  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-566-076-12

Alignment Scores:  
Pred. No.: 1,15e-08 Length: 2466  
Score: 204.50 Matches: 143  
Percent Similarity: 36.35% Conservative: 94  
Best Local Similarity: 21.93% Mismatches: 214  
Query Match: 5.13% Indels: 201  
DB: 4 Gaps: 29

US-09-502-945-5 (1-2162) x US-09-566-076-12 (1-2466)

QY 1 CTGGCGCGGTCCGGTCCGGGCTCTT----- 27

Db 991 ProProGlnThrValAlaGluLeuValGlyLysProSerHisGlnMetSerArgSer 1010

QY 28 ---TCCAGCTCTCGCAGCCGGCCACCCGAAGAAACGGGTCGTGCAACAGCACCGCTGGA 84  
Db 1011 AspAlaGluSerLeuAlaGlyValThrLysLeuAsnAsnSerLysSerValAla----- 1028  
QY 85 CTGGCCCGCAGCATGAGCGGAAAGTGGCCCGAGAAATTCGGCATAAGGTGATTTCTGT 144  
Db 1029 -----SerLeuAsnArgSerProGluArgArg---LysHisGluSerAspSerSer 1044  
QY 145 ATTGAATAATGATGACAGAAAGGACTATCTCTATGATGTGTCGGAATGTACCAACAGACC 204  
Db 1045 SerIleGluAspProGlyGlnAlaTyrValLeuAspValLeu-----HisLysArg 1061  
QY 205 ATGGACGTGGCGCTGCTCGTGGGAGACCTGGAAGCTGGTCAATCAATGAACCCAGCCGCTGTG 264  
Db 1062 TrpSer-----IleValSerSerProGluArg--- 1070  
QY 265 CCTCTGTTTGTATGTCGCGCTGATCCACCTGATCCACCTGAAGTACCAGGTGGAATATGATCAG 324  
Db 1071 -----GluIleThrLeuValAsnLeuLysLysAspAlaLysTyr----- 1083  
QY 325 CTGACCCCGCGCGCTCCAGGAAGCTGAAGGAGTGGCTTGGACCGTCTGCACCCCGAA 384  
Db 1083 ----- 1083  
QY 385 GGCTCGCGCTGAGTGTGCTGCTGGCTGGCTGGAGTTTGGC-----TGTGGGCTTTC 435  
Db 1084 GlyLeuGlyPheGlnIleIleGlyGlyLysMetGlyArgLeuAspLeuGlyIlePhe 1103  
QY 436 ATCTCCACCTCATCAAGCGGTGAGGAGCAGCAGCGTCTGG-----CTCAGGTAGGGGAC 492  
Db 1104 IleSerSerValAlaProGlyGlyProAlaAspPheHis3LysLeuLysProGlyAsp 1123  
QY 493 GAGATCGTCGGATCAATGGATATTCATCTCTCTGTACCCCATGAGGAGGTCAAC 552  
Db 1124 ArgLeuIleSerValAsnSerValSerLeuGluGlyValSerHisHisAlaIleGlu 1143  
QY 553 CTCATTTCGAACCAAGAAACCTGTGTCCATCAAGTGAGACACATCGGCTGATCCCCGTG 612  
Db 1144 IleLeu----- 1145  
QY 613 AAAAGCTCTCTGTATGAGCCCTCCTACTTGGCAGTATGTGATCAGTTTGTGTGCGAATCT 672  
Db 1146 GlnAsnAlaProGluAsp-----ValThrLeuValIleSerGlnPro 1159  
QY 673 GGGGGCGTCGAGGCGACGCTGGGCTCCCTCGAAATCGG3AAAAACAAGGAGGAAGGTC 732  
Db 1160 -----LysGluLys----- 1162  
QY 733 TTCATCAGCTGTGTAGGCTCCCGAGGCTTGGCTGCAGCATTTCCAGCGGCCCATCCAG 792  
Db 1163 ---IleSer-----LysValProSerThrProValHis 1172  
QY 793 AAGCTTGGCATCTTTATCATGCCATGTGAACCTGGCTCCCTGTCTGTCTGAGTGGGATGTG 852  
Db 1173 LeuThrAsnGluMetLysAsnTyrMetLysSerSer----- 1185  
QY 853 GAGATAGGGGACGAGATTCTCGAAGTCAATGGCTGCGACTTCTTAACCTGGATCAAG 912  
Db 1186 -----TyrMetGlnAspSerAlaIleAspSerSerLysAspHisHis 1200  
QY 913 GAGGCTGTAATGTCTGTAATAATAGCCGCGACCTGACCATCTCCATTGTAGCTGAGCT 972  
Db 1201 TrpSerArgGlyThrLeu-----ArgHisIleSerGluAsnSerPheGlyProSer 1217  
QY 973 GGC-----CGGAGCTGTTCATGACAGACCGGGAGCGCTGGCAGAGCGCGGCGGCGGT 1026  
Db 1218 GlyGlyLeuArgGluGlySerLeuSerSerGlnAspSerArgThrGluSerAlaSerLe 1237  
QY 1027 GAGCTGCAGC-----GGCAGGAGCTTCTCATGCAGAACCGG-----TGGCGATG 1071  
Db 1237 userGlnSerGlnValAsnGlyPhePheAlaSerHisLeuGlyAspGlnThrTrpGlnG 1257  
QY 1072 GAGTCCAAACAGATCCTCCAGGAGCAGCAGGAGATGGAC CGGCAAAAGGAGAAAGAAATT 1131

```
Db 1257 user-GlnHisGlySerProSerProSerValIleSerLysAlaThrGluLysGluThrP 1277
QY 1132 GCCAAGGCGACAGAGGAAATGAGATACCGGAA---GGAGATGGAACAGATTGT- 1187
Db 1277 heThrAspSerAsnGlnSerLysThrLysLysProGlyLysAspValThrAspTyrS 1297
QY 1188 -----AGAGGAGGAGAGAGTATTAGAGCAATGGGAAGACAGTGGGGCTCAAGGAA 1242
Db 1297 erAspArgGlyAspSerAspMetAspGluAla-----T 1308
QY 1243 CAGCTACTCTTGCTAAACCATCACTGCTGAGGTACACCCAGTACCCCTTCGCAAGCCA 1302
Db 1308 hrTyrSerSerGlnAspHisGln-----ThrProLysGlnGluSerSerS 1325
QY 1303 AAGTGATTTCCGGAATATAGGAAGGCTTTGACCCCTACTCTATCTTCCACCCAGCA 1362
Db 1325 erValAsnThrSerAsn--LysMetAsnPhelysThrPheSerSerProProLysPr 1344
QY 1363 GATCATGGGAGGATGTCGGGCTCTCAGCATCAAGAGGAGGATCCTTAGACCTGGC 1422
Db 1344 o-----GlyAspIlePheGluValGluLeuAlaLysAsnAspAsnSerLeuGlyIleSe 1362
QY 1423 CTGGAAGGCGGTGACTCCCCATT-----GGAGGTGGTCTCTCTCTGTGTA 1476
Db 1362 rValThrGlyGlyValAsnThrSerValArgHisGlyGlyIleTyrValIleAlaValI 1382
QY 1477 TGAGCGGGAGCTGCTGAGCGGCATGTGGCATTTGAAAGGGGAGGAGATCATGGCAAT 1536
Db 1382 eProGlnGlyAlaAlaGluSerAspGlyArgIleHisLysGlyAspArgValleuAlaVa 1402
QY 1537 CAACGCAAGATTGTGACAGACTACACCTGGCTGAGGTGAGCTGAGCTGCCCTG----- 1588
Db 1402 laeGlyValSerLeuGlyAlaThrHisLysGlnAlaValGluThrLeuArgAsnTh 1422
QY 1588 ----- 1588
Db 1422 rGlyGlnValValHisLeuLeuGluLysGlyGlnSerProThrSerLysGluHisVa 1442
QY 1589 -----CAGAAGCGCTGGAAATCAGGCGGGGAGCTG 1617
Db 1442 lProValThrProGlnCysThrLeuSerAspGlnAsnAlaGlnGlyGlnGlyProGluL 1462
QY 1618 GATCGACCTGTGGTGGCTGCGCTGCCCCCAAGAGGAGTATGAC-----GATGAGCT 1668
Db 1462 sValLysLysThrThrGlnVal-----LysAspTyrSerPheValThrGluGluAs 1479
QY 1669 GACCTTC-----TTGCTGAGTCCAAAGGGGAAACCAATTCACGCGTTAGGAA 1719
Db 1479 nThrPheGluValLysLeuPheLysAsnSerSerGlyLeuGlyPheSerPheSerArgGl 1499
QY 1720 CAGTGAGCTCCGGCCCCCACCCTCGTGAAC 1747
Db 1499 uAspAsnLeuIleProGluGlnIleAsn 1508
```

## RESULT 15

PCT-US94-09943-2

; Sequence 2, Application PC/TUS9409943

; GENERAL INFORMATION:

; APPLICANT:

; APPLICANT:

; APPLICANT:

; APPLICANT:

; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL

; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN

; NUMBER OF INVENTION: TYROSINE PHOSPHATASES

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; STREET: 600 ATLANTIC AVENUE

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09943
; FILING DATE: 01-SEP-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: TWOMEY, MICHAEL J.
; REGISTRATION NUMBER: P-38,349
; REFERENCE/DOCKET NUMBER: LO461/7000WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; TELEX: 92-1742 EZBKIL
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2466 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-09943-2
```

```
Alignment Scores:
Pred. No.: 1,158-08 Length: 2466
Score: 204.50 Matches: 143
Percent Similarity: 36.35% Conservative: 94
Best Local Similarity: 21.93% Mismatches: 214
Query Match: 5.13% Indels: 201
DB: 5 Gaps: 29
```

US-09-502-945-5 (1-2162) x PCT-US94-09943-2 (1-2466)

```
QY 1 CCTGGCCCGCTCGGTGCGGCTCTT----- 27
Db 991 ProProGlnThrValAlaGluLeuValGlyLysProSerHisGlnMetSerArgSer 1010
QY 28 ---TCAGGTCTGGCAGCGCGGCCAGGAGCGGTGTCGCAACACGACGAGTGA 84
Db 1011 AspAlaGluSerLeuAlaGlyValThrLysLeuAsnAsnSerLysSerValAla----- 1028
QY 85 CTGGCCCGACCATGACCGCAAAAGTGGCCCGAGAAATCCCGCATAAAGTGGATTCTG 144
Db 1029 -----SerLeuAsnArgSerProGluArg-----LysHisGluSerAspSer 1044
QY 145 ATTGAAATGATGCAGAGAGGACTATCTATGATGCTGCGAATGTACCAACGAGACC 204
Db 1045 SerIleGluAspProGlyGlnAlaTyrValLeuAspValLeu-----HisLysArg 1061
QY 205 ATGGAGCTGGCGCTGCTGCTGGGAGACCTGAAGCTGTCAATCAATGAACCCAGCCCTCTG 264
Db 1062 TrpSer-----IleValSerSerProGluArg--- 1070
QY 265 CCTCTGTTTGATGCCATTCGGCGGTGATCCCACTGAAGCACCAGGTGGATATGATCAG 324
Db 1071 -----GluIleThrLeuValAsnLeuLysLysAspAlaLysTyr----- 1083
QY 325 CTGACCCCGCGCTGCCAGGAAGTGAAGAGGTGCGTCTGGACCGTCTGCACCCCGAA 384
Db 1083 ----- 1083
QY 385 GGCCTCGGCTGAGTGTGCTGGTGGTGGCTCGGAGTTTGGC-----TGTGGGCTCTTC 435
Db 1084 GlyLeuGlyPheGlnIleIleGlyGlyGlyLysMetGlyArgLeuAspLeuGlyIlePhe 1103
QY 436 ATCTCCACCTCATCAAGGCGGTGAGGAGACAGCGTCCGG---CTCCAGGTAGGGGAC 492
Db 1104 IleSerSerValAlaProGlyGlyProAlaAspPheHisGlyCysLeuLysProGlyAsp 1123
```

